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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:20:41 ; Search time 11 Seconds
(without alignments)
227.215 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72

Perfect score: 231
Sequence: 1 RKAMKGLGTDEESILTLTIS.....ISAAPKTLFGRIIDLDIKSE 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	231	100.0	319 1 ANX5_HUMAN	P08758 homo sapien
2	224	97.0	320 1 ANX5_BOVIN	P81287 bos taurus
3	207	89.6	319 1 ANX5_MOUSE	P48036 mus musculu
4	206	89.2	321 1 ANX5_CHICK	P17153 gallus galli
5	194	84.0	318 1 ANX5_RAT	P14668 rattus norv
6	179	77.5	323 1 ANX5_CYNPY	P70075 cynops pyr
7	173	74.9	318 1 ANX4_BOVIN	P13214 bos taurus
8	172	74.5	318 1 ANX4_PIG	P08132 sus scrofa
9	170	73.6	618 1 ANX6_BOVIN	P79134 bos taurus
10	169	73.2	463 1 ANX7_MOUSE	Q07076 mus musculu
11	167	72.3	318 1 ANX7_MOUSE	P09525 homo sapien
12	167	72.3	672 1 ANX6_HUMAN	P08133 homo sapien
13	166	71.9	318 1 ANX6_CHICK	P51901 gallus galli
14	165	71.4	318 1 ANX4_CANFA	P50994 canis fam1
15	164	71.0	672 1 ANX6_MOUSE	P14824 mus musculu
16	163	70.6	318 1 ANX7_MOUSE	P55260 rattus norv
17	163	70.6	466 1 ANX7_HUMAN	P20073 homo sapien
18	162	70.1	318 1 ANX4_MOUSE	P97429 mus musculu
19	162	70.1	672 1 ANX6_RAT	P48037 rattus norv
20	159	68.8	503 1 ANXB_BOVIN	P27214 bos taurus
21	159	68.8	503 1 ANXB_MOUSE	P97384 mus musculu
22	159	68.8	503 1 ANXB_RABIT	P31477 corytolagus
23	159	68.8	505 1 ANXB_HUMAN	P50995 homo sapien
24	156	67.5	316 1 ANXC_HYDAT	P26256 hydat atten
25	150	64.9	327 1 ANX8_HUMAN	P13928 homo sapien
26	150	64.9	327 1 ANX8_MOUSE	Q092125 xenopus lae
27	149.5	64.7	512 1 ANX7_XENLA	O92125 xenopus lae
28	148	64.1	324 1 ANX3_DROME	P22465 drosophila
29	141	61.0	320 1 ANX3_DROME	P22465 drosophila
30	131	56.7	323 1 ANX3_HUMAN	P12429 homo sapien
31	129	55.8	323 1 ANX3_MOUSE	Q35639 mus musculu
32	124	53.7	324 1 ANX3_RAT	P14669 rattus norv
33	120	51.9	462 1 ANX7_DICDI	P24639 dicystostell

34	119	51.5	345 1 ANX1_RAT
35	118	51.1	345 1 ANX1_MOUSE
36	116	50.2	345 1 ANX1_HORSE
37	115	49.8	314 1 ANX4_PRRAN
38	115	49.8	315 1 ANXO_CANFA
39	112	48.5	338 1 ANX2_BOVIN
40	112	48.5	333 1 ANI2_COLL1
41	111	48.1	338 1 ANX2_HUMAN
42	111	48.1	338 1 ANX2_MOUSE
43	111	48.1	338 1 ANX2_RAT
44	111	48.1	346 1 ANX1_RABIT
45	110	47.6	324 1 ANXA_HUMAN

ALIGNMENTS

RESULT 1	ID	ANX5_HUMAN	STANDARD;	PRT;	319 AA.
AC	P08758;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PAP-1) (Thromboplasticin inhibitor) (Vascular anticoagulant-alpha) (Anchoring CII)				
GN	ANXAS OR ANXS OR ENX2 OR PP4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=88234495; PubMed=2967495;				
RX	Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F., Kuepper H.;				
RA	"Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).				
RL	[2]				
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RP	MEDLINE=88271329; PubMed=2455636;				
RX	Wauter-Fogt I., Reutelingersperger C.P.M., Pieters J., Bodo G., Strizlowa C., Hauptmann R.;				
RA	"Cloning and expression of cDNA for human vascular anticoagulant, a Ca2+-dependent phospholipid-binding protein.";				
RT	Eur. J. Biochem. 174:585-592(1988).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=88273202; PubMed=2968983;				
RX	Peponsky R.B., Tizard R., Matelliano R.J., Sinclair L.K., Miller G.T., Brownig J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter I.				
RA	Hession C., Frey A.Z., Wallner B.P.;				
RT	"Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";				
RL	J. Biol. Chem. 263:10799-10811(1988).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=88163463; PubMed=2964863;				
RA	Funkhosh T., Hendrickson L.E., McMillen B.A., Fujikawa K.;				
RT	"Primary structure of human placental anticoagulant protein.";				
RL	Biochemistry 26:8087-8092(1987).				
RN	[5]				
RP	SEQUENCE FROM N.A., AND SEQUENCE.				
RX	MEDLINE=88139278; PubMed=2963810;				
RA	Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y., Arai K., Iwaguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T., Shidara Y., Murata M., Maki M.;				
RT	"Structure and expression of cDNA for an inhibitor of blood coagulation isolated from human placenta: a new lipocortin-like protein.";				

P07150	rattus r
P10107	mus musc
Q8hzm6	equus ca
P51074	fragaria
Q29471	canis fa
P04272	bos tau
Q92040	columba
P07355	homo sap
P07356	mus mus
Q07936	rattus
P51652	oryzocol
Q9u712	homo sa

RL J. Biochem. 102:1261-1273(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca²⁺ and
RL phospholipid binding protein.";
RN J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
RL MEDLINE=95047484; PubMed=7958999;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
RL high G+C content.";
RN Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RL Tait J.F.;
RT "Organization of the human annexin V (ANX5) gene.";
RN Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, Ovary, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RL Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RL Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RL Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RL Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RL Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Parley U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RL Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RL Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rothhut R., Comera C., Cortial S., Haumont P.-Y., Diep Le K.H.,
RL Cavadore J.-C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
RL identical with the placental inhibitor of blood coagulation.";
RN Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130; 258-296 AND 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Mehlman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
RL calcium- and phospholipid-binding protein.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=8906652; PubMed=2974032;
RA Ann N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
RL de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RL phospholipase A2 inhibitors from human placenta. Evidence against a
RL mechanistically relevant association between enzyme and inhibitor.";
RN J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
RL anticoagulant protein that binds to calcium and membranes.";
RN EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
RT analysis at 2.0-A resolution. Implications for membrane binding and
RL calcium channel activity.";
RN FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92117413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RL Luecke H., Roemisch J., Paques E.-P.;
RT "Crystal and molecular structure of human annexin V after refinement.
RT Implications for structure, membrane binding and ion channel
RL formation of the annexin family of proteins.";
RN J. Mol. Biol. 223:683-704(1992).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=98062349; PubMed=9398511;
RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
RT "Crystal structure of annexin V with its ligand K-201 as a calcium
RL channel activity inhibitor.";
RN J. Mol. Biol. 274:16-20(1997).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98118533; PubMed=9435213;
RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
RT "Residue-specific bioincorporation of non-natural, biologically
RT active amino acids into proteins as possible drug carriers: structure
RL and stability of the per-thioproline mutant of annexin V.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
RN [18]
RP FUNCTION: This protein is an anticoagulant protein that acts as an
RL indirect inhibitor of the thromboplastin-specific complex, which
RL is involved in the blood coagulation cascade.
CC -!- SUBUNIT: Monomer. Binds ANX (By similarity).
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- SIMILARITY: Belongs to the annexin family.
CC -!- SIMILARITY: Contains 4 annexin repeats.
CC -!- CAUTION: This protein has been independently sequenced by at least
CC seven groups under different names!
CC -!- DATABASE: NMR-BD Systems' cytokine source book: Annexin 5;
CC WWW="http://www.rndsystems.com/asp/9_sitebuilder.asp?bodyid=185".
CC
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CC
DR EMBL: X13454; CAI0985.1; -
DR EMBL: M13984; AAB5545.1; -
DR EMBL: M1366; AAA3570.1; -
DR EMBL: M21731; AAA3616.1; -
DR EMBL: D00172; BAA00122.1; -
DR EMBL: J03745; AAA52386.1; -
DR EMBL: U01691; AAB40047.1; -
DR EMBL: U01681; AAB40047.1; JOINED.
DR EMBL: U01682; AAB40047.1; JOINED.
DR EMBL: U01683; AAB40047.1; JOINED.
DR EMBL: U01685; AAB40047.1; JOINED.
DR EMBL: U01686; AAB40047.1; JOINED.
DR EMBL: U01687; AAB40047.1; JOINED.
DR EMBL: U01689; AAB40047.1; JOINED.
DR EMBL: U01690; AAB40047.1; JOINED.

Query Match	100.0%	Score 231;	DB 1;	Length 319;
Best Local Similarity	100.0%	Pred. No. 9, 2e-21;		
Matches	48;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

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Oy      1  RKAMKGTDEESILTLTTRSNAQOEISAFTLLFGRLDDDKSE 48
Db      24  RKAMKGTDEESILTLTTRSNAQOEISAFTLLFGRLDDDKSE 71

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RESULT 2	
ANX5_BOVIN	
ID	ANX5_BOVIN
	STANDARD;
	PRT;
	320 AA

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (C8B-1) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplasmin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Annexin CII).
GN ANX5 OR ANX5.
OS Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RC TISSUE=Brain; MEDLINE=93041974; PubMed=1420335;
 RX Leamonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y.,
 RA Giambanco I., Bianchi R., Puta G., Ceccarelli P., Donato R.,
 RA Green B.N., Altchen A.,
 RT "Novel isoforms of Cabp 33/37 (annexin V) from mammalian brain:
 RT structural and phosphorylation differences that suggest distinct
 RT biological roles.";
 RL Biochim. Biophys. Acta 1160:76-83 (1992).
 CC -1- FUNCTION: This protein is an anticoagulant protein that acts as
 CC an indirect inhibitor of the thromoplastin-specific complex,
 CC which is involved in the blood coagulation cascade.
 CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

DR HSSP, P08758; 1ANW.
DR InterPro: IPRO01464; Annexin.
DR Pfam: PF00191; annexin_4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin_4.
DR SMART: SM00335; ANX_4.
DR PROSITE: PS00223; ANNEXIN_4.
DR Annexin, Calcium/phospholipid-binding; Repeat; Blood coagulation, KW Acetylation.

Query Match	97.0%;	Score 224;	DB 1;	Length 320;
Best Local Similarity	95.8%;	Pred. No: 6.5e-20;		
Matches	46;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0;

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QY      1 :RKAMKGLTDEESILTLTTSRSNAQOEISAEKTLFGRDLDDDKSE 48
      |||||
Db      24 RKAMKGLTDEESILTLTTSRSNAQOEIAVAEFTLFGRLDDDKSE 71

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RESULT	3				
ANX5_MOUSE					
ID	ANX5_MOUSE	STANDARD;	PRT;	319	AA

DT	01-FEB-1996 (Rel. 33, Created)	
DT	01-FEB-1996 (Rel. 33, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Annexin CII) .	
DE	ANXAS OR ANXS.	
GN	Mus musculus (Mouse) .	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_TaxID=10090;	

RP	SEQUENCE FROM N.A.	
RQ	STRAIN=129/SvJ; TISSUE=Liver;	
RX	MEDLINE=99072820; PubMed=9854034;	
RA	Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,	
RB	Fernandez M.P.;	
RT	Mouse annexin V genomic organization includes an endogenous	
RT	retrovirus. "; 7:125-131(1999).	
RL	J. Blochem. 337:125-131(1999).	
CC	-1- FUNCTION: This protein is an anticoagulant protein that acts as	
CC	indirect inhibitor of the thromboplaetin-specific complex, which	
CC	is involved in the blood coagulation cascade.	
CC	-1- SUBUNIT: Monomer. Binds ATRK (by similarity).	
CC	-1- DOMAIN: A pair of annexin repeats may form one binding site for	
CC	calcium and phospholipid.	
CC	-1- SIMILARITY: Belongs to the annexin family.	
CC	-1- SIMILARITY: Contains 4 annexin repeats.	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/ann	
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CC
DR EMBL; U29396; AAC52530.1; -.
DR EMBL; D63423; BAA09728.1; -.
DR EMBL; AJ230108; CAA13092.1; JOINED.
DR EMBL; AJ230110; CAA13092.1; JOINED.
DR EMBL; AJ230111; CAA13092.1; JOINED.
DR EMBL; AJ230114; CAA13092.1; JOINED.
DR EMBL; AJ230116; CAA13092.1; JOINED.
DR EMBL; AJ230118; CAA13092.1; JOINED.
DR EMBL; AJ230119; CAA13092.1; JOINED.
DR EMBL; AJ230120; CAA13092.1; JOINED.
DR EMBL; AJ230121; CAA13092.1; JOINED.
DR EMBL; AJ230122; CAA13092.1; JOINED.
DR EMBL; AJ230123; CAA13092.1; JOINED.
DR EMBL; AJ230124; CAA13092.1; JOINED.
DR HSSP; P14668; 1AB8.
DR SWISS-2DPAGE; P48036; MOUSE.
DR MGD; MGI:106008; Anxa5.

```

DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR PRODOM: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KM Placenta.
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2E1C36B7 CRC64;
 Query Match 89.6%; Score 207; DB 1; Length 319;
 Best Local Similarity 87.5%; Pred. No. 7.6e-18;
 Matches 42; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRAMKGLGTDEESILTLTFRSNAQOEISAAFKTLFGDLDDLKSE 48
 DB 23 RRAMKGLGTDEESILTLTFRSNAQOEISAAFKTLFGDLDDLKSE 70
 RESULT 4
 ANX5 CHICK STANDARD; PRT; 321 AA.
 ID ANX5 CHICK STRAND; PRT; 321 AA.
 AC P17153;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchotin CII).
 DE (Anchotin CII).
 GN ANX5 OR ANX5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 [1]
 RN RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88186917; PubMed=2833522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfeaffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of anchotin CII, a collagen binding protein isolated from chondrocyte membrane.";
 RL J. Biol. Chem. 263:5921-5925 (1988).
 [2]
 RN RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=90020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.;
 RT "Alternative splicing or cloning artefact?";
 RL Trends Biochem. Sci. 14:325-325 (1989).
 [3]
 RN RP REVISIONS.
 RX MEDLINE=90243721; PubMed=2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfeaffle M.,
 RA Deutzmann R., Mollenhauer J., von der Mark K.;
 RT "The structure of anchotin CII, a collagen binding protein isolated from chondrocyte membrane.";
 RL J. Biol. Chem. 265:8344-8344 (1990).
 [4]
 RN RP REVISIONS.
 RX MEDLINE=94215900; PubMed=8163186;
 RA Yamada Y., Garrone R., von der Mark K.;
 RL EMBO J. 9:1336-1336 (1990).
 [5]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Liver;
 RX MEDLINE=94215900; PubMed=8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.;
 RT "Structure of the gene encoding anchotin CII (chick annexin V).";

RL Gene 141:179-186 (1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=93249384; PubMed=8484740;
 RA Boustead C.M., Brown R., Walker J.H.;
 RT "Isolation, characterization and localization of annexin V from chicken liver.";
 RL Biochem. J. 291:601-608 (1993).
 [7]
 RN RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93229489; PubMed=8471604;
 RA Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.;
 RT "Structure of chicken annexin V at 2.25-A resolution.";
 RL Biochemistry 32:3923-3929 (1993).
 CC -1- FUNCTION: Collagen-binding protein.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 CC EMBL; M30971; AAA48591.1; ALT_SEQ.
 CC EMBL; U01680; AAB39917.1; JOINED.
 CC EMBL; U01671; AAB39917.1; JOINED.
 CC EMBL; U01672; AAB39917.1; JOINED.
 CC EMBL; U01673; AAB39917.1; JOINED.
 CC EMBL; U01675; AAB39917.1; JOINED.
 CC EMBL; U01676; AAB39917.1; JOINED.
 CC EMBL; U01677; AAB39917.1; JOINED.
 CC EMBL; U01678; AAB39917.1; JOINED.
 CC EMBL; U01679; AAB39917.1; JOINED.
 CC PIR; A35381; LUC45.
 CC PDB; 1ALA; 31-OCT-93.
 CC InterPro: IPR001464; Annexin.
 CC Pfam: PF00191; annexin; 4.
 CC PRINTS: PR00196; ANNEXIN.
 CC PRODOM: PD000143; Annexin; 4.
 CC SMART: SM00335; ANX; 4.
 CC PROSITE: PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 KM Annexin.
 FT REPEAT 24 84 ANNEXIN 1.
 FT REPEAT 96 156 ANNEXIN 2.
 FT REPEAT 180 240 ANNEXIN 3.
 FT REPEAT 255 315 ANNEXIN 4.
 FT CONFLICT 168 168 D -> E (IN REF. 1).
 FT TURN 13 14
 FT HELIX 17 28
 FT HELIX 35 44
 FT HELIX 47 61
 FT HELIX 65 72
 FT HELIX 75 85
 FT TURN 88 90
 FT HELIX 91 100
 FT HELIX 107 116
 FT HELIX 119 133
 FT HELIX 137 144
 FT HELIX 147 157
 FT TURN 158 158
 FT HELIX 169 184
 FT TURN 185 187
 FT HELIX 191 200
 FT HELIX 203 217
 FT HELIX 221 224
 FT HELIX 232 245
 FT HELIX 247 259

FT HELIX 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SO SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;

Query Match 89.2%; Score 206; DB 1; Length 321;
 Best Local Similarity 83.3%; Pred. No. 1e-17;
 Matches 40; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

db 1 RKAMKGLTDEESITLTTSRNMQRQISAFKTLFERRDLDLXSE 48
 25 RKAMKGLTDEETIKITTSRNMQRQISAFKTLFERRDLDLXSE 72

RESULT 5
 ID ANX5_RAT STANDARD; PRT; 318 AA.

AC P14668;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A5 (Annexin V) (lipocortin V) (Endonexin II) (Calphobindin I)
 DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANX5 OR ANX5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88273202; PubMed=2968983;
 RA Pedinsky R.B., Tizard R., Mataliano R.J., Sinclair L.K.,
 Miller G.T., Browning J.L., Chow E.P., Byrne C., Huang K.S.,
 Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
 RA "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I.";
 RT J. Biol. Chem. 263:10799-10811 (1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=96035863; PubMed=7556178;
 RA Imai Y., Kohsaka S.;
 RT "Structure of rat annexin V gene and molecular diversity of its
 RT transcripts.";
 RT Eur. J. Biochem. 232:327-334 (1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=93369587; PubMed=8362244;
 RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
 RT changes.";
 RT Science 261:1321-1324 (1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC TISSUE=Kidney;
 RX MEDLINE=96069783; PubMed=7583670;
 RA Swaitio M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
 RT the membrane-binding protein annexin V.";
 RT Nat. Struct. Biol. 2:968-974 (1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
 RX MEDLINE=98272673; PubMed=9609693;
 RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swaitio M.A., Balch C.,
 Head J.F., Retzinger G., Dedman J.R., Seaton B.A.;
 RT "Mutational and crystallographic analyses of interfacial residues in
 RT annexin V suggest direct interactions with phospholipid membrane
 RT components.";
 RT Biochemistry 37:8004-8010 (1998).

EN [6]
 RP INTERACTION WITH DNMT1.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=96301899; PubMed=8667030;
 RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;
 RT "Molecular cloning and characterization of annexin V-binding protein
 RT with highly hydrophilic peptide structure.";
 RT J. Neurochem. 67:89-97 (1996).
 RL FUNCTION. This protein is an anticoagulant protein that acts as
 indirect inhibitor of the thromboplastin-specific complex, which
 is involved in the blood coagulation cascade.
 CC -1 SUBUNIT: Monomer. Binds ATRX and DNMT1.
 CC -1 DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1 SIMILARITY: Belongs to the annexin family.
 CC -1 SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M21730; AAA41512.1; -;
 DR EMBL; D42137; BAA07708.1; -;
 DR EMBL; D42129; BAA07708.1; JOINED.
 DR EMBL; D42132; BAA07708.1; JOINED.
 DR EMBL; D63337; BAA07708.1; JOINED.
 DR EMBL; D42131; BAA07708.1; JOINED.
 DR EMBL; D42132; BAA07708.1; JOINED.
 DR EMBL; D42133; BAA07708.1; JOINED.
 DR EMBL; D42134; BAA07708.1; JOINED.
 DR EMBL; D42135; BAA07708.1; JOINED.
 DR EMBL; D42136; BAA07708.1; JOINED.
 DR EMBL; D42136; BAA07708.1; JOINED.
 DR PIR; C29250; LURT5.
 DR PDB; 2RAN; 30-NOV-94.
 DR PDB; 1A8A; 17-JUN-98.
 DR PDB; 1A8B; 17-JUN-98.
 DR PDB; 1BC0; 13-JAN-99.
 DR PDB; 1BC1; 13-JAN-99.
 DR PDB; 1BC2; 13-JAN-99.
 DR PDB; 1BC3; 13-JAN-99.
 DR PDB; 1BCW; 13-JAN-99.
 DR PDB; 1BCY; 13-JAN-99.
 DR PDB; 1BCZ; 13-JAN-99.
 DR PDB; 1GSN; 13-MAR-02.
 DR PDB; 1N41; 04-FEB-03.
 DR PDB; 1N42; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR PDB; 1N44; 04-FEB-03.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin.4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin.4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN.4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KW Placenta; Acetylation; 3D-structure.
 KW INT. MET 0
 FT REPEAT 20 80 ANNEXIN 1.
 FT REPEAT 92 152 ANNEXIN 2.
 FT REPEAT 176 236 ANNEXIN 3.
 FT REPEAT 251 311 ANNEXIN 4.
 FT MOD. RES 1 1 ACETYLATION.
 FT TURN 10 11
 FT HELIX 14 25
 FT HELIX 32 39
 FT TURN 40 41
 FT HELIX 44 58
 FT HELIX 62 69
 FT HELIX 72 82
 FT HELIX 85 97
 FT HELIX 104 113

FT HELIX 116 130
 FT HELIX 134 141
 FT HELIX 144 154
 FT TURN 155 156
 FT HELIX 166 179
 FT TURN 180 182
 FT HELIX 188 197
 FT HELIX 200 214
 FT HELIX 218 225
 FT HELIX 228 242
 FT HELIX 244 256
 FT HELIX 263 273
 FT TURN 274 277
 FT HELIX 278 289
 FT HELIX 293 300
 FT HELIX 303 313
 SQ SEQUENCE 318 AA, 35613 MW, 1A755A7C11FA11CE CRC64;

Query Match 84.0%; Score 194; DB 1; Length 318;
 Best Local Similarity 79.2%; Pred. No. 2.9e-16;
 Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

1 RKAMKGLGTEDESIITLLTFRSNAORQETSAFKTLFGDLDLDDKSE 48
 22 RKAMKGLGTEDESIITLLTFRSNAORQETSAFKTLFGDLDLDDKSE 69

RESULT 6

ANX5_CYNPY STANDARD; PRT; 323 AA.
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hikono T., Abe S.I.;
 RT "Differential expression of annexin V during spermatogenesis in the
 RT newt *Cynops pyrrhogaster*.";
 RL Dev. Genes Evol. 206:64-71(1996).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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EMBL; D44134; BA01012.1; -
 DR HSSP; P08758; IAHV.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR K01 Annexin; Calcium/phospholipid-binding; Repeat.
 REPEAT 26 86 ANNEXIN 1.
 FT REPEAT 98 158 ANNEXIN 2.
 FT REPEAT 182 242 ANNEXIN 3.

FT REPEAT 257 317 ANNEXIN 4.
 SQ SEQUENCE 323 AA, 35981 MW, 044B31AC2816ACE2 CRC64;

Query Match 77.5%; Score 179; DB 1; Length 323;
 Best Local Similarity 75.0%; Pred. No. 1.9e-14;
 Matches 36; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

1 RKAMKGLGTEDESIITLLTFRSNAORQETSAFKTLFGDLDLDDKSE 48
 27 RKAMKGLGTEDESIITLLTFRSNAORQETSAFKTLFGDLDLDDKSE 74

RESULT 7

ANX4_BOVIN STANDARD; PRT; 318 AA.
 AC P13214;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
 DE (P4-X) (35-Beta calcitriol) (Carbohydrate-binding protein P33/P41)
 DE (P33/41).
 GN ANX4 OR ANX4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=99050088; PubMed=2847715;
 RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
 RT "Cloning and characterization of a cDNA encoding bovine endonexin
 RT (chromobindin 4).";
 RL Biochem. Biophys. Res. Commun. 156:660-667(1988).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96205957; PubMed=8631806;
 RA Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
 RT "Characterization of carbohydrate-binding protein p33/41: relation
 RT with annexin IV, molecular basis of the doublet forms (p33 and p41),
 RT and modulation of the carbohydrate binding activity by
 RT phospholipids.";
 RL J. Biol. Chem. 271:7679-7685(1996).
 RL [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA Sutton R.B., Sprang S.R.;
 RL Submitted (SEP-1995) to the PDB data bank.
 RL [4]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RX MEDLINE=98070213; PubMed=9405281;
 RA Zanotti G., Malpegi G., Glubich F., Foll C., Stoppini M., Oliva L.,
 RA Savio A., Berni R.;
 RT "Structure of the trigonal crystal form of bovine annexin IV.";
 RL Biochem. J. 329:101-106(1998).
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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EMBL; M22248; AAA30507.1; -

DR EMBL: X13627; CAA31954.1; -
 DR EMBL: D78178; BAA11243.1; -
 DR PIR: A31578; LUBO4.
 DR PDB: 1ANN; 29-JUN-96.
 DR PDB: 1AOW; 14-JUN-98.
 DR PDB: 1IAW; 25-APR-01.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SMO0335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 KW ANNEXIN; 1.
 FT INIT MET 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 94 94 L -> V (IN REF. 2).
 FT CONFLICT 210 210 E -> K (IN REF. 2).
 FT HELIX 15 26
 FT HELIX 33 40
 FT TURN 41 42
 FT HELIX 45 59
 FT HELIX 63 70
 FT HELIX 73 83
 FT HELIX 86 98
 FT HELIX 105 114
 FT HELIX 117 131
 FT HELIX 135 142
 FT HELIX 145 155
 FT HELIX 156 166
 FT TURN 167 182
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT HELIX 264 274
 FT HELIX 275 278
 FT TURN 279 290
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBDF349D774FD CRC64;
 Query Match 74.9%; Score 173; DB 1; Length 318;
 Best Local Similarity 70.8%; Pred. No. 1e-13; 8; Indels 0; Gaps 0;
 Matches 34; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKAMKGLGTDSESLITLTSRSNAQROEISAAFKTLFGRDLDDKSE 48
 DB 23 RKAMKGLGTDDEALIVLAAYRSTQROEIRYAVKTTIGRDLMDLKS 70
 RESULT 8
 ANX4 PIG STANDARD; PRT; 318 AA.
 AC P08132; Q29306;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4)
 DE (Protein II) (P32.5) (Placental anticoagulant protein I) (PAV-II)
 DE (PP4-X) (35-beta calcimedlin).
 GN ANX4 OR ANX4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestinal epithelium;
 RX MEDLINE=87275850; PubMed=2956093;

RA Weber K., Johnson N., Plesmann U., Van P.N., Soling H.-D., Ampe C.
 RA Vanderkerckhove J.;
 RT "The amino acid sequence of protein II and its phosphorylation site
 RT for protein kinase C; the domain structure Ca²⁺-modulated lipid
 RT binding proteins.";
 RL EMBO J. 6:1599-1604 (1987).
 RN [2]
 RP SEQUENCE OF 1-126 FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm W., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine CDNA
 RT library: analysis of 839 clones.";
 RL Mamm. Genome 7:509-517 (1996).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC
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 CC
 DR EMBL: F14682; CAA23194.1; -
 DR PIR: A27107; LUPG4.
 DR HSSP: P13214; 1ANN.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PF00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SMO0335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KW Acetylation.
 FT INIT MET 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT MOD_RES 1 1 ACETYLATION (PROBABLE).
 FT MOD_RES 6 6 PHOSPHORYLATION (BY PKC).
 SQ SEQUENCE 318 AA; 35697 MW; FA7D9CE2B76C31B8 CRC64;
 Query Match 74.5%; Score 172; DB 1; Length 318;
 Best Local Similarity 70.8%; Pred. No. 1.3e-13; 7; Indels 0; Gap
 Matches 34; Conservative 7; Mismatches 7; Indels 0; Gap
 QY 1 RKAMKGLGTDSESLITLTSRSNAQROEISAAFKTLFGRDLDDKSE 48
 DB 23 RKAMKGLGTDDEALIVLAAYRSTQROEIRYAVKTTIGRDLMDLKS 70
 RESULT 9
 ANX6 BOVIN STANDARD; PRT; 618 AA.
 ID ANX6 BOVIN
 AC P79134;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CFB-II)
 DE (Fragment).
 GN ANX6 OR ANX6.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Camera C., Creutz C.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=96422308; PubMed=9748523;
 RA Avila-Sakar A.J., Creutz C.E., Kretsinger R.H.;
 RL "Crystal structure of bovine annexin VI in a calcium-bound state";
 RT Biochim. Biophys. Acta 1387:103-116(1998).
 CC -!- FUNCTION: May associate with CD21. May regulate the release of
 CC Ca(2+) from intracellular stores.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- PTM: Phosphorylated in response to growth factor stimulation (by
 CC similarity).
 CC -!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; U87539; AAB47570.1; -.
 DR PDB; IAVC; 28-JAN-98.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin. 8.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 8.
 DR SMART; SM00335; ANX; 8.
 DR PROSITE; PS00223; ANNEXIN; 6.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
 KW 3D-structure.
 FT NON_TER 1 1
 FT REPEAT <1 34 ANNEXIN 1.
 FT REPEAT 46 106 ANNEXIN 2.
 FT REPEAT 130 190 ANNEXIN 3.
 FT REPEAT 205 265 ANNEXIN 4.
 FT REPEAT 317 377 ANNEXIN 5.
 FT REPEAT 389 449 ANNEXIN 6.
 FT REPEAT 478 538 ANNEXIN 7.
 FT REPEAT 553 613 ANNEXIN 8.
 FT HELIX 1 11
 FT HELIX 15 22
 FT HELIX 26 35
 FT HELIX 38 50
 FT HELIX 57 66
 FT HELIX 69 83
 FT HELIX 87 92
 FT TURN 93 94
 FT TURN 97 97
 FT HELIX 98 108
 FT HELIX 119 132
 FT TURN 133 135
 FT HELIX 141 150
 FT HELIX 153 167
 FT HELIX 171 175
 FT TURN 176 177
 FT HELIX 181 195
 FT HELIX 197 209
 FT HELIX 216 225
 FT TURN 226 230
 FT HELIX 231 241
 FT HELIX 246 253

FT HELIX 256 266
 FT HELIX 278 293
 FT TURN 306 307
 FT HELIX 310 319
 FT TURN 320 321
 FT HELIX 328 335
 FT TURN 336 337
 FT HELIX 340 354
 FT HELIX 358 365
 FT HELIX 368 378
 FT HELIX 381 392
 FT TURN 393 393
 FT HELIX 400 407
 FT TURN 408 409
 FT HELIX 412 425
 FT HELIX 430 437
 FT HELIX 440 449
 FT TURN 450 451
 FT HELIX 461 474
 FT HELIX 491 498
 FT HELIX 501 515
 FT HELIX 519 526
 FT HELIX 529 556
 FT TURN 557 557
 FT HELIX 564 573
 FT TURN 574 578
 FT HELIX 579 590
 FT HELIX 594 601
 FT HELIX 604 614
 FT TURN 615 615
 SO SEQUENCE 618 AA; 69796 MW; 5571F70F24B5836F CRC64;
 Query Match 73.6%; Score 170; DB 1; Length 618;
 Best Local Similarity 68.8%; Pred. No. 4.6e-13;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 RKAMKGLTDEESITLTLRSNAQRETSAPKTLFGRLDPLKSE 48
 Db 318 RKAMKGLTDEETITLITLRSNAQROQIRQTKSHRGRLMDLNSK 365
 |||||:::|||||:::|||||
 RESULT 10
 ANX7_MOUSE STANDARD; PRT; 463 AA.
 ID ANX7_MOUSE
 AC 007076;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A7 (Annexin VII) (Synexin).
 GN ANX7 OR ANX7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93168121; PubMed=7916616;
 RA Zhang-Keck Z.Y., Burns A.L., Pollard H.B.;
 RT "Mouse synexin (annexin VII) polymorphisms and a phylogenetic
 RT comparison with other synexins.";
 RL Biochem. J. 289:735-741(1993).
 CC -!- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis.
 CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -!- SIMILARITY: Belongs to the annexin family.
 CC -!- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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CC EMBL; L13129; AAA37238.1; -
 CC HSSP; P28256; 1DM5.
 DR MGD; MGI:88031; Anx4.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat.
 FT DOMAIN 1 143 REPEAT-RICH REGION.
 FT REPEAT 169 229 ANNEXIN 1.
 FT REPEAT 241 301 ANNEXIN 2.
 FT REPEAT 324 384 ANNEXIN 3.
 FT REPEAT 400 460 ANNEXIN 4.
 FT DOMAIN 5 20 3 X 5 AA TANDEM REPEATS OF G-Y-P-P-X.
 FT REPEAT 5 9 1.
 FT REPEAT 10 14 2.
 FT REPEAT 16 20 3.
 SQ SEQUENCE 463 AA; 49939 MW; 50F7B20FD48EBDC5 CRC64;

Query Match 73.2%; Score 169; DB 1; Length 463;
 Best Local Similarity 64.6%; Pred. No. 4, 5e-13;
 Matches 31; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

1 RRAMGGLTDEESITLTLSRNSAQROEISAFKTLFGRLDLDKSE 48
 170 RRAMGFGTDEQIVDVVSNRNDORQIKAFKTMGKDLKDKSE 217

RESULT 11

ANX4 HUMAN STANDARD; PRT; 318 AA.
 ID ANX4 HUMAN P09525; Q96F33; Q9BWK1;
 AC P09525; Q96F33; Q9BWK1; Created
 DT 01-MAR-1989 (Rel. 10, 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (Pp-X) (35-beta calcimedlin) (Carbohydrate-binding protein P3/P41) (P33/41).
 DE ANX4 OR ANX4.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX (1)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=8309022; PubMed=2970257;
 RA Grundmann U., Amani E., Abel K.-J., Kuepper H.A.;
 RT "Isolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family."
 RL Behring Inst. Mitt. 82:59-67(1988).
 RN (2)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92155721; PubMed=1346776;
 RA Distche C.M.;
 RT Tait J.F., Smith C., Frankenherry D.A., Miao C.H., Adler D.A.,
 RL "Chromosomal mapping of the human annexin IV (ANX4) gene";
 RN Genomics 12:313-318(1992).

RP SEQUENCE FROM N.A.
 RP MEDLINE=97239215; PubMed=9084877;
 RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
 RA Matsuno I.;
 RT "Characterization of human p33/41 (annexin IV), a Ca²⁺ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, A31 and A317";
 RT Biol. Pharm. Bull. 20:224-229(1997).
 RN [4]

RP SEQUENCE FROM N.A.
 RC TISSUE=Eye, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,
 RA Richards A.C., Wozley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettman M., Madan A.C., Shvachenko Y., Bouffard G.G.,
 RA Whitting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez J.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 26-55; 98-123 AND 279-307.
 RP MEDLINE=8906652; PubMed=2974032;
 RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
 RA J. Biol. Chem. 263:18657-18663(1988).
 RT "Sedimentation equilibrium analysis of five lipocortin-related phospholipase A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor."
 RL [6]
 RN SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
 RP MEDLINE=89118212; PubMed=2975506;
 RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
 RA Hendrickson L.E., Fujikawa K.;
 RT "Placental anticoagulant proteins: isolation and comparative characterization four members of the lipocortin family."
 RL Biochemistry 27:6268-6276(1988).
 RN [7]
 RN X-RAY CRYSTALLOGRAPHY.
 RP MEDLINE=91073383; PubMed=2254922;
 RA Freeman P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
 RT "Crystallization and preliminary X-ray crystallographic studies of human placental annexin IV."
 RL J. Mol. Biol. 216:219-221(1990).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
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CC EMBL; M19383; AAC41689.1; ALT INIT.
 CC EMBL; M82809; AAA51740.1; -
 CC EMBL; D78152; BAA11227.1; ALT INIT.
 CC EMBL; BC000182; AAH00182.1; ALT INIT.
 CC EMBL; BC011659; AAH11659.1; ALT INIT.
 CC PIR; A42077; A42077.
 CC HSSP; P13214; IANN.
 CC SWISS-2DPAGE; P09525; HUMAN.
 CC PMMA-2DPAGE; P09525; -
 CC Genew; HGNC:542; ANX4.

MIM; 106491; -
 DR InterPro; IPRO01464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 FT INIT MET 0 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 95 95 R -> O (IN REF. 1).
 SQ SEQUENCE 318 AA; 35751 MW; 16B19E01500350F7 CRC64;

Query Match 72.3%; Score 167; DB 1; Length 318;
 Best Local Similarity 66.7%; Pred. No. 5 4e-13;
 Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

1 RRAMGLTDESIITLTLSNAQROFISAFAKTLFGRLDLDLXSE 48
 23 RRAMGLTDEDAISVLAHYRTAQRQEIPTAYKSTIGRLDLDLXSE 70

RESULT 12

ANK6_HUMAN STANDARD; PRT; 672 AA.

AC P08133;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANX6 OR ANX6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88196081; PubMed=3258820;
 RA Crumpson M.R., Owens R.J., Totty N.F., Moss S.E., Waterfield M.D.,
 RT Crumpson M.J.;
 RT "Primary structure of the human, membrane-associated Ca2+-binding
 RT protein p68 a novel member of a protein family.";
 RL EMBO J. 7:21-27(1988).

RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88124902; PubMed=2963335;
 RA Suedhof T.C., Staughter C.A., Leznicki I., Barton P., Reynolds G.A.;
 RT "Human 67-kDa calelectrin contains a duplication of four repeats
 RT found in 35-kDa lipocortins";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).

RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89380132; PubMed=2528541;
 RA Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T.,
 RA Saito Y., Shidara Y., Maki M.;
 RT "Structure and expression of cDNA for calphobindin II, a human
 RT placental coagulation inhibitor.";
 RL J. Biochem. 106:43-49(1989).

RN [4]
 RP SEQUENCE.
 RX MEDLINE=90236978; PubMed=2139657;
 RA Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
 RT "Structure and properties of calphobindin II, an anticoagulant
 RT protein from human placenta.";
 RL J. Biochem. 107:43-50(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=uterus;

RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McKernan P.J., Winkler J., Green E.D., Dickson M.C.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Genetic and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[6]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
 RX MEDLINE=96326697; PubMed=8709144;
 RA Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann S.,
 RA Huber R., Voges D.;
 RT "The structure of recombinant human annexin VI in crystals and
 RT membrane-bound.";
 RL J. Mol. Biol. 260:638-643(1996).

CC -1- FUNCTION: May associate with CD21. May regulate the release of
 CC Ca(2+) from intracellular stores.
 CC -1- INDUCTION: By EBV.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 8 annexin repeats.

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CC
 DR EMBL; D00510; BAA00400.1; -
 DR EMBL; Y00097; CAA68286.1; -
 DR EMBL; J03578; AAA35656.1; -
 DR EMBL; BC017046; AAH17046.1; -
 DR PIR; J00032; AOH068.
 DR PDB; 1W91; 15-APR-03.
 DR Genew; HGNC:544; ANXA6.
 DR MIM; 114070; -
 DR InterPro; IPRO01464; Annexin.
 DR Pfam; PF00191; annexin; 8.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 8.
 DR SMART; SM00335; ANX; 8
 DR PROSITE; PS00223; ANNEXIN; 8.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Acetylation;
 KW Phosphorylation; 3D-structure.
 FT INIT MET 0 0
 FT REPEAT 28 88 ANNEXIN 1.
 FT REPEAT 100 160 ANNEXIN 2.
 FT REPEAT 184 244 ANNEXIN 3.
 FT REPEAT 259 319 ANNEXIN 4.
 FT REPEAT 371 431 ANNEXIN 5.
 FT REPEAT 443 503 ANNEXIN 6.
 FT REPEAT 532 592 ANNEXIN 7.
 FT REPEAT 607 667 ANNEXIN 8.
 FT MOD_RES 1 1 ACETYLATION.

FT CONFLICT 225 226 IE -> MK (IN REF. 2).
FT CONFLICT 554 554 S -> T (IN REF. 2).
FT CONFLICT 618 618 E -> D (IN REF. 1).
SQ SEQUENCE 672 AA; 75742 MW; 2829237029BDIDCB CRC64;

Query Match 72.3%; Score 167; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 1.2e-12;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 RKAMGIGTDEESITLLTGRSNAOROEISAPKTLFGRLDLDKSE 48
Db 372 RKAMGIGTDEEDITLITRHSNVRQOIRQTFKSHRGRLMDPKSE 419

RESULT 13
ANX6_CHICK STANDARD; PRT; 671 AA.

AC P51901;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
GN ANX6 OR ANX6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94092130; PubMed=8267590;
RA Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.;
RT "Characterization, cloning and expression of the 67-kDa annexin from
RT chicken growth plate cartilage matrix vesicles."
RL Biochem. Biophys. Res. Commun. 197:556-561(1993).
CC -1- FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 8 annexin repeats.

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CC or send an email to license@isb-sib.ch).

CC EMBL; S67466; AAB29337.2; -
DR PTR; JC2029; JC2029.
DR HSSP; P79134; IAVC.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 5.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT REPEAT 27 87 ANNEXIN 1.
FT REPEAT 99 159 ANNEXIN 2.
FT REPEAT 183 243 ANNEXIN 3.
FT REPEAT 258 318 ANNEXIN 4.
FT REPEAT 370 430 ANNEXIN 5.
FT REPEAT 442 502 ANNEXIN 6.
FT REPEAT 531 592 ANNEXIN 7.
FT REPEAT 607 666 ANNEXIN 8.
SQ SEQUENCE 671 AA; 75218 MW; D0E02F4311A93D98 CRC64;
Query Match 71.9%; Score 166; DB 1; Length 671;
Best Local Similarity 70.8%; Pred. No. 1.5e-12;

Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 RKAMGIGTDEESITLLTGRSNAOROEISAPKTLFGRLDLDKSE 48
Db 371 RKAMGIGTDEGALIEVLGRSNAOROEIKAYKAYHGRDLDKSE 418

RESULT 14
ANX4_CANFA STANDARD; PRT; 318 AA.

AC P50994;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A4 (Annexin IV) (lipocortin IV) (36 kDa zymogen granule
DE membrane associated protein) (ZAP36).
GN ANX4 OR ANX4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Carnivora; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 78-95 AND 134-149.
RX STRAIN=Mongrel; TISSUE=Pancreas;
RX MEDLINE=22015264; PubMed=12020832;
RA Fukuko S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.;
RT "Cloning and characterization of ZAP36, an annexin-like, zymogen
RT granule membrane associated protein, in exocrine pancreas."
RL Biochim. Biophys. Acta 1575:148-152(2002).
RN [2]
RP SEQUENCE OF 1-9.
RX MEDLINE=94362286; PubMed=7765250;
RA Fukuko S.-I.;
RT "Analysis of ZAPs, zymogen granule membrane associated proteins, in
RT the regulated exocytosis of the pancreas."
RL Biosci. Biotechnol. Biochem. 58:1282-1285(1994).
CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
CC (By similarity).
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.

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CC or send an email to license@isb-sib.ch).

CC EMBL; D38223; BAA07398.1; -
DR HSSP; P13214; IANN.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT MET 0
FT REPEAT 22 82 ANNEXIN 1.
FT REPEAT 94 154 ANNEXIN 2.
FT REPEAT 178 238 ANNEXIN 3.
FT REPEAT 253 313 ANNEXIN 4.
FT CONFLICT 138 138 V -> D (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 318 AA; 35681 MW; 42EFSB8917984863 CRC64;
Query Match 71.4%; Score 165; DB 1; Length 318;
Best Local Similarity 64.6%; Pred. No. 9.5e-13;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDSEILTLTTSRNSNAQROEISAAFKTLFGRLDLDLXSE 48
DB 23 RKAMKGLGTDSEILTLTTSRNSNAQROEISAAFKTLFGRLDLDLXSE 70

Search completed: April 8, 2004, 11:57:13
Job time: 11 secs

RESULT 15

ANX6_MOUSE STANDARD; PRT; 672 AA.
ID ANX6_MOUSE
AC P14824;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
GN ANXA6 OR ANX6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=89010687; PubMed=2972541;
RA Moss S.E., Crumpton M.R., Crumpton M.J.;
RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
RT lipocortin family";
RL Bur. J. Biochem. 177:21-27 (1988).
CC -1- FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 8 annexin repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X13460; CAA31808.1; -.
DR PIR: S01786; S01786.
DR HSSP: P79134; IAVC.
DR MGD: MGI:88255; Anxa6.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 8.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 8.
DR SMART: SM00335; ANX; 8.
DR PROSITE: PS00223; ANNEXIN; 8.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INIT MET 0
FT REPEAT 28 88 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
SQ SEQUENCE 672 AA: 75755 MW; 2D85C1DD235FC76 CRC64;

Query Match 71.0%; Score 164; DB 1; Length 672;

Best Local Similarity 66.7%; Pred. No. 2.7e-12;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDSEILTLTTSRNSNAQROEISAAFKTLFGRLDLDLXSE 48
DB 372 RKAMKGLGTDSEILTLTTSRNSNAQROEISAAFKTLFGRLDLDLXSE 419

CC amino acid sequences. They are also useful for preventing, treating or
CC ameliorating medical conditions, such as cancer, neurodegenerative
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,
CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or
CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).
CC Sequences ABG9888-ABG9989 and ABU0010-ABU0433 represent human
CC polypeptides of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office

CC Sequence 117 AA;

Query Match 100.0%; Score 231; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMGLGTDESIITLLTSSNAQREISAFTLFGRLDDPKSE 48
DB 25 RKAMGLGTDESIITLLTSSNAQREISAFTLFGRLDDPKSE 72

RESULT 2

AA13592 standard; protein; 146 AA.

AA13592;

25-MAR-2003 (revised)
30-SEP-1991 (first entry)

PAP-I-protein C fusion construct.

Phospholipid; binding protein; lipocortin; domain; vitamin K; PAP;
gla-domain; VKDP.

Homo sapiens.

Location/Qualifiers
1.136
/label= PAP-I

Protein
137.140
/label= protein C
/note= "amino acids 46-49"

Misc-difference
141.146
/label= LYS, ARG

MO9109953-A.

11-JUL-1991.

29-DEC-1989; 89US-00459082.

29-DEC-1989; 89US-00459082.

(ZYMO) ZYMOGENETICS INC.

Foster DC;

WPI, 1991-222905/30.

N-PSDB; AAQ12681.

Recombinant prodn. of hybrid phospholipid-binding proteins - comprising
lipocortin phospholipid-binding domain and vitamin-K-dependent protein.

Claim 21; Page 41; 57pp; English.

The fusion was constructed using site-directed mutagenesis to fuse PAP-I
encoding amino acid 1-136 with a protein C DNA sequence at the codon for
amino acid 46. A plasmid contg. this construct was transfected into BHK
cells which were then cultured to produce PAP-I-protein C fusions which
were activated to a form fully active in both amidolytic and

CC anticoagulant assays. This sequence contains and additional fragment of
CC amino acids Lys or Arg, between the light and heavy chains. At least
CC three amino acids are present. See also AAQ12678-81. (Updated on 25-MAR-
CC 2003 to correct PA field.)

CC Sequence 146 AA;

Query Match 100.0%; Score 231; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMGLGTDESIITLLTSSNAQREISAFTLFGRLDDPKSE 48
DB 24 RKAMGLGTDESIITLLTSSNAQREISAFTLFGRLDDPKSE 71

RESULT 3

AA58393 standard; protein; 208 AA.

AA58393;

14-MAR-2001 (first entry)

Lung cancer associated polypeptide sequence SEQ ID 731.

Human; lung cancer associated protein; neuroprotective; cytosolic;
cardioactive; immunomodulatory; muscular active; vulnery;
gastrointestinal; nephrotropic; antiinfective; gynecological;
antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
proliferative disorder; wound healing; infectious disease.

Homo sapiens.

WO20005180-A2.

21-SEP-2000.

08-MAR-2000; 2000WO-US005918.

12-MAR-1999; 99US-0124270P.

(HUMA-) HUMAN GENOME SCI INC.

(ROSEN/) ROSEN C A.

Ruben SM;

WPI, 2000-587514/55.

N-PSDB; AAF18269.

Lung cancer associated gene sequences, referred to as lung cancer
antigens, useful for treatment, prevention, and diagnosis of disorders
such as lung cancer.

Claim 11; Page 1248-1249; 1425pp; English.

Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
associated proteins represented in AAB58106 - AAB58548. Lung cancer
associated proteins and polynucleotide sequences, their agonists, and
antagonists may have neuroprotective, cytosolic, cardioactive;
immunomodulatory; muscular active general; vulnery; gastrointestinal
general; nephrotropic; antiinfective; gynecological; or antibacterial
activity. The invention also includes antibodies specific for the protein
or polynucleotide sequences. The lung cancer associated polynucleotide
sequences may be used for detection of lung cancer, chromosome
identification, as chromosome markers, and for numerous other diagnostic
or research purposes. The proteins may be used to treat disorders such as
neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
cardiovascular, renal, and proliferative disorders. The proteins may also
be used in the treatment of wounds and infectious diseases.
Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
used in the course of the invention for the identification and
characterisation of the polynucleotide and protein sequences

XX Sequence 208 AA;

Query Match 100.0%; Score 231; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 48
28 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 75

RESULT 4
AAR26276
ID AAR26276 standard; protein; 319 AA.

AC AAR26276;
XX
DT 10-MAR-2003 (revised)
DT 04-FEB-1993 (first entry)

DE CPB-I.
XX CPB-I; stabilisation; frozen; molten; processed; activity.

XX Homo sapiens.

XX JP04198195-A.

XX 17-JUL-1992.

XX 28-NOV-1990; 90JP-00328286.

XX 28-NOV-1990; 90JP-00328286.

XX (KOMA) KOMA CO LTD.

XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-288937/35.

XX Stabilisation of CPB-I for drug compsn. - by adding basic aminoacid

XX selected from lysine, arginine and/or ornithine.

XX Disclosure; Page 2; 4pp; Japanese.

XX The sequence given is the amino acid sequence of CPB-I. CPB-I was used

XX within a method which involved adding basic amino acids to it which

XX resulted in its stabilisation. This lead to the production of CPB-I which

XX keeps its activity when it is frozen, molten or has been processed by

XX several procedures. (Updated on 10-MAR-2003 to add missing OS field.)

XX Sequence 319 AA;

QY 1 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 48
24 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 71

RESULT 5
AAR26180
ID AAR26180 standard; protein; 319 AA.

XX AAR26180;

XX 10-MAR-2003 (revised)

XX 04-FEB-1993 (first entry)

XX CPB-1.

KW CPB-1; saccharides; stabilisation; antihemagglutination; dermal disea

XX corneal disease.

XX Homo sapiens.

XX JP04198196-A.

XX 17-JUL-1992.

XX 28-NOV-1990; 90JP-00328287.

XX 28-NOV-1990; 90JP-00328287.

XX (KOMA) KOMA CO LTD.

XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.

XX WPI; 1992-288938/35.

XX Stabilisation of CPB-1 for drug compsn. - contains saccharide select

XX from glucose, glucosamine, xylose, saccharose and/or dextran,

XX Disclosure; Page 2; 4pp; Japanese.

XX The sequence given is the amino acid sequence of CPB-1. CPB-1 was us

XX within the method of the invention which involved adding saccharides

XX it which resulted in its stabilisation. The saccharide was pref. glu

XX glucosamine, xylose, saccharose, or dextran. This lead to the product

XX of CPB-1 which kept its activity when it had been processed by sever

XX treatments. CPB-1 can be used as a medicine for antihemagglutination

XX dermal and corneal diseases. (Updated on 10-MAR-2003 to add missing

XX field.)

XX Sequence 319 AA;

QY 1 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 48
24 RKAMKGLGTDEESITLTLTSRSNAQROEISAFAFTLFGRLDLDKSE 71

RESULT 6
AAR41021
ID AAR41021 standard; protein; 319 AA.

XX AAR41021;

XX 29-MAR-1994 (first entry)

XX Calphobindin I (CPB-I).

XX Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.

XX Homo sapiens.

XX JP05213769-A.

XX 24-AUG-1993.

XX 04-FEB-1992; 92JP-00019032.

XX 04-FEB-1992; 92JP-00019032.

XX (KOMA) KOMA CO LTD.

XX (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKITSUHO.

XX WPI; 1993-299558/38.

XX Protein kinase C inhibitor effective against malignant tumours - CC

XX (opt. recombinant) calphobindin I.

PS Claim 1; Page 2-3; 6pp; Japanese.
XX
CC Calphobindin I (CPB-1) or recombinant calphobindin I (r-CPB-1) inhibits
CC protein kinase C (PKC) and is useful in the treatment of malignant
CC tumors caused by abnormal activation of PKC. CPB-1 is extracted from
CC human or animal organs and may be applied intravenously, orally,
CC intramuscularly, percutaneously or rectally.
XX
SQ Sequence 319 AA;

Query Match 100.0%; Score 231; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTTSRNSAORISAPKTLFGRLDLDLKDSE 48
DB 24 RKAMKGLGTDEESILTLTTSRNSAORISAPKTLFGRLDLDLKDSE 71

RESULT 7
ABG32550
ID ABG32550 standard; protein; 319 AA.

AC ABG32550;
DT 29-NOV-2002 (first entry)

DE Human CPB-1 protein.

XX Human; CPB-1; eye drop; ophthalmological; aneixin V; corneal disease;
XX calcium/phospholipid binding protein; polyhydric alcohol.

OS Homo sapiens.

PN WO200267977-A1.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WO-JP001563.

PR 26-FEB-2001; 2001JP-00050297.

PA (KOMA) KOMA CO LTD.

XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

PI Naruse H, Sano M, Shinoda Y, Inagi T;

DR WPI; 2002-674988/72.

PT Eye drops for treating e.g. corneal diseases, contain CPB-1 and
PT polyhydric alcohol with specific carbonyl value, without unpleasant
PT irritation upon dropping but with satisfactory long-term storability.
XX
XX Disclosure; Page 13-14; 16pp; Japanese.

CC The invention relates to eye drops contain CPB-1 (aneixin V) and a
CC polyhydric alcohol having a carbonyl value of not more than 5micro
CC Mol./g. The eyes drops are for treating e.g. corneal diseases. Such eye
CC drops are without unpleasant irritation upon dropping but with
CC satisfactory long-term storage stability. The present sequence is the
CC human CPB-1 (calcium/phospholipid binding) protein
XX
XX Sequence 319 AA;

Query Match 100.0%; Score 231; DB 5; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTTSRNSAORISAPKTLFGRLDLDLKDSE 48
DB 24 RKAMKGLGTDEESILTLTTSRNSAORISAPKTLFGRLDLDLKDSE 71

RESULT 8
ADE55088
ID ADE55088 standard; protein; 319 AA.
XX
XX ADE55088;

DT 29-JAN-2004 (first entry)

DE Human Protein P08758, SEQ ID NO 893.

XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNL; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

PI Woolf C, D'Urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; P08758.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNL)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 319 AA;

Query Match 100.0%; Score 231; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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XX AC AAP80511;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-2003 (revised)
XX DT 12-NOV-1990 (first entry)
XX DE Placental coagulation inhibitor.
XX KM Placental coagulation inhibitor; disseminated vascular coagulation;
XX KM thrombosis.
XX OS Homo sapiens.
XX PN EP279459-A.
XX PD 24-AUG-1988.
XX PF 19-FEB-1988; 88EP-00102468.
XX PR 20-FEB-1987; 87JP-00037227.
XX PR 23-JUL-1987; 87JP-00184428.
XX PA (KOMA ) KOMA CO LTD.
XX PI Saino Y, Iwasaki A, Suda M,
XX DR WPI; 1988-236733/34.
XX DR N-PSDB; AAN81113.
XX PT Recombinant placental coagulation inhibitor - useful for the prevention
XX PT and treatment of thromboses or disseminated intravascular coagulation.
XX PS Disclosure; Page ?; 31pp; English.
XX XX
XX CC This polypeptide exhibits strong anticoagulant activities and is useful
XX CC for the treatment and prevention of e.g. thrombosis or disseminated
XX CC intravascular coagulation in the brain, heart and peripheral blood
XX CC vessels, such as cerebral and myocardial infarction. It has no
XX CC antigenicity against man and can be produced in large amts. using
XX CC recombinant methods. (Updated on 10-MAR-2003 to add missing OG field.)
XX CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
XX CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 320 AA;

Query Match          100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAMKGLGTDESIITLTLTSRSNAQROEISAAFKTLFGRLDDDKSE 48
DB 25 RRAMKGLGTDESIITLTLTSRSNAQROEISAAFKTLFGRLDDDKSE 72

RESULT 12
AAP80242
ID AAP80242 standard; protein; 320 AA.
XX AC AAP80242;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 12-SEP-1990 (first entry)
XX DE Sequence vascular anticoagulating protein (VAP) VAC-alpha (Asp22).
XX KM Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
XX KM antiinflammatory; phospholipase inhibitory.
XX OS Homo sapiens.
XX PN MO8807576-A.
XX XX

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PD PD 06-OCT-1988.
XX PF 26-MAR-1988; 88WO-EP000266.
XX XX
XX PR 28-MAR-1987; 87DE-03710309.
XX PR 28-MAR-1987; 87DE-03710364.
XX PR 28-MAR-1987; 87DE-03710430.
XX PR 04-NOV-1987; 87DE-03737367.
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX XX
XX PI Hauptmann R, Maurerfogy I, Bodo G, Sweetly P, Stratowa C;
XX PI Falkner E, Adole G, Reutlingsp CMP;
XX XX
XX DR WPI; 1988-292861/41.
XX DR N-PSDB; AAN80872.
XX XX
XX PT New vascular anti-coagulating proteins - useful as thrombin inhibitors,
XX PT antiinflammatory agents, etc.
XX XX
XX PS Claim 41; Page 171-72; 183pp; German.
XX XX
XX CC The DNA is produced by determining the amino acid sequence of isolated
XX CC and highly purified VAPs, constructing DNA probes on the basis of this
XX CC sequence, using the probes to search through suitable cDNA libraries,
XX CC isolating cDNA that hybridises with the probes, by inserting the cDNA
XX CC into a suitable vector, and using the vector to transform a host
XX CC organism. VAC-alpha has anticoagulant activity under certain conditions,
XX CC but loses this activity in the event of severe bleeding. It acts by
XX CC inhibiting conversion of factor X to factor Xa and conversion of
XX CC prothrombin to thrombin. It is structurally related to lipocortin I
XX CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
XX CC has similar antiinflammatory and phospholipase inhibitory activity.
XX CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX CC correct PA field.)
XX SQ Sequence 320 AA;

Query Match          100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAMKGLGTDESIITLTLTSRSNAQROEISAAFKTLFGRLDDDKSE 48
DB 25 RRAMKGLGTDESIITLTLTSRSNAQROEISAAFKTLFGRLDDDKSE 72

RESULT 13
AAP90053
ID AAP90053 standard; protein; 320 AA.
XX AC AAP90053;
XX XX
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 01-NOV-1989 (first entry)
XX DE anticoagulant PP4 protein.
XX KM Anticoagulant; PP4 protein; thromboplasticin.
XX OS Homo sapiens; (human).
XX PN EP318703-A.
XX PD 07-JUN-1989.
XX XX
XX PF 29-OCT-1988; 88EP-00118039.
XX PR 03-NOV-1987; 87DE-03737239.
XX PA (BEHW ) BEHRINGER AG.
XX XX

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PI Grundmann U, Abel KU, Kupper H;
XX WPI, 1989-16767/23.
XX
XX New DNA sequence encoding anticoagulant P4 protein - and new recombinant
PT protein, vectors, antibodies, etc., useful therapeutically and
PT diagnostically.
XX
XX Claim 1, Page 11 and Table 1; 12pp; German.
XX
XX Amino acid sequence of anticoagulant P4 protein. This inhibits blood
CC coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 320 AA;

Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 48
DB 25 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 72

RESULT 14

AAP91363
ID AAP91363 standard; protein; 320 AA.

AC AAP91363;

DT 22-DEC-1989 (first entry)

DE Human lipocortin-V.

KM Human lipocortin-V; lambdaHLipo V-1; anti-inflammatory agent.

OS Homo sapiens.

PN EP30396-A.

PD 30-AUG-1989.

PF 20-FEB-1989; 89BP-00301603.

PR 26-FEB-1988; 88US-00160866.

PA (BIOJ) BIOGEN INC.

PI Wallner BP, Pepinsky RB, Browning JL;

DR WPI, 1989-250486/35.

PT Human lipocortin cpds. III, IV, V, and VI - used in treatment of
PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders
PT involving inflammatory processes.

PS Claim 16; Fig 4; 32pp; English.

XX Human lipocortin-V was isolated from a lambda gt10 human peripheral blood
CC lymphocyte cDNA library with rat lipocortin-V cDNA of lambda Rlipo V-1 as
CC probe. Lipocortins are anti-inflammatory agents and can be used to treat
CC arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See
CC also AAN90598, AAN90599, and AAP91362

SQ Sequence 320 AA;

Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 48
DB 25 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 72

RESULT 15

AAP91953
ID AAP91953 standard; protein; 320 AA.

AC AAP91953;

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 30-JUL-1989 (first entry)

DE Vascular anti-coagulating protein-alpha.

KM Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.

OS Homo sapiens.

OS Chimeric.

PN DE3810331-A.

PD 05-OCT-1989.

PF 26-MAR-1988; 88DE-03810331.

PR 26-MAR-1988; 88DE-03810331.

PA (BOEH) BOEHRINGER INGELHEIM.

PI Gunther A;

DR WPI, 1989-293724/41.

DR N-PSDB; AAN91353.

PT Monoclonal antibodies to vascular anti-coagulating proteins - and
PT hybridomas producing such antibodies.

PS Disclosure; Fig 1; 11pp; German.

XX This vascular anti-coagulating protein (VAC)-alpha is used in the
CC preparation of monoclonal antibodies (mAbs). The VAC-alpha is injected
CC into a host animal, in conjugation with eg keyhole limpet haemocyanin
CC and the B-cells from immunised hosts are then fused with myeloma cells
CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to
CC alpha. Abs can be used as immunoassay reagents to detect VAC protein
CC affinity ligands for protein purification, and as medicaments for binding
CC and/or neutralising VAC proteins in vivo. See also AAN91354 and BP-
CC 181465. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise
CC field)

SQ Sequence 320 AA;

Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 48
DB 25 RKAMKGLGTDEESITLTLSRSNAQROEISAAFKTLFGRLDLDLKSE 72

Search completed: April 8, 2004, 11:56:50
Job time : 56 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:50:30 ; Search time 20 Seconds
(without alignments)
230.860 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72
Perfect score: 231
Sequence: 1 RKMKGIGTDEBSILTLTFS.....ISAAPKTLFGRIIDLDKSE 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	231	100.0	320 1 AOHUP	annexin V [validat
2	224	97.0	320 1 S27214	annexin V - bovine
3	206	89.2	321 1 LURHS	annexin V - chicke
4	194	84.0	319 1 LURHS	annexin V - rat
5	173	74.9	319 1 LURHS	annexin IV - bovin
6	172	74.5	318 1 LURHS	annexin IV - pig
7	169	73.2	463 2 S29170	annexin VII - mous
8	167	72.3	321 1 A42077	annexin IV [valida
9	167	72.3	673 1 AOHU68	annexin VI [valida
10	166	71.9	157 2 S09020	annexin VII - chick
11	166	71.9	671 2 JC2029	annexin VI - mouse
12	164	71.0	673 1 S01786	annexin VII, long
13	163	70.6	488 1 LURHS	annexin VI - rat
14	162	70.1	673 1 S52844	annexin XI form A
15	159	68.8	503 1 LURHS	annexin XI form B
16	159	68.8	503 1 LURHS	annexin XI form B
17	159	68.8	505 2 S23447	annexin XI - human
18	159	68.8	505 2 A53152	annexin XI - human
19	156	67.5	316 1 LURHS	annexin XII - Hydr
20	150	64.9	327 1 LURHS	annexin VII - hum
21	149.5	64.9	512 2 S70644	annexin VII - Atri
22	148	64.1	296 1 LURHS	annexin IX - fruit
23	142	61.5	676 2 S41022	hypothetical prote
24	141	61.0	321 1 LURHS	annexin X - fruit
25	131	56.7	323 1 LURHS	annexin III - huma
26	124	53.7	324 1 LURHS	annexin III - rat
27	120	51.9	462 1 LURHS	annexin VII - slim
28	119	51.5	346 1 LURHS	annexin I - rat
29	118	51.1	346 1 LURHS	annexin I - mouse

30	115	49.8	316 2 A57076	annexin XIIa -
31	115	49.8	321 2 A84809	probable annexi
32	115	49.8	357 2 B57076	annexin XIIb -
33	112	48.5	339 1 LURHS	annexin II - bo
34	112	48.5	343 1 A44118	annexin I type
35	111	48.1	339 1 LURHS	annexin II - hu
36	111	48.1	339 1 LURHS	annexin II - mo
37	111	48.1	339 1 LURHS	annexin II - ra
38	111	48.1	339 2 S53700	annexin II - gu
39	110	47.6	346 1 LURHS	annexin XII, 1
40	109	47.2	316 1 LURHS	annexin I - hum
41	108	46.8	346 1 LURHS	annexin, isofo
42	104	45.0	315 2 T06322	annexin I - ch
43	102	44.2	130 2 S36103	annexin I - bo
44	102	44.2	346 1 S28228	annexin I typ
45	100	43.3	340 1 JQ1298	annexin II typ

ALIGNMENTS

RESULT 1
AOHUP
annexin V [validated] - human
N/Alternate names: endonexin II, lipocortin V, placental
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-20
C/Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C319
R/Peptide, R.B.; Tizard, R.; Matalliano, R.J.; Sinclair, L.K.; Miller, G
U/Biol. Chem. 263, 10799-10811, 1988
A/Title: Five distinct calcium and phospholipid binding proteins share ho
A/Reference number: A29250; A28076; MUID:88273202; PMID:2968983
A/Accession: D29250
A/Molecule type: mRNA
A/Residues: 1-320 <PDB>
A/Cross-references: GB:M1731; NID:9186969; PIDN:AAA36166.1; PID:9307116
R/Grundmann, U.; Abel, K.J.; Bohm, H.; Loebmann, H.; Lottspeich, F.; Ku
Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988
A/Title: Characterization of cDNA encoding human placental anticoagulant
A/Reference number: A30206; MUID:88234495; PMID:2967495
A/Accession: A30206
A/Molecule type: mRNA
A/Residues: 1-320 <GRU>
A/Cross-references: GB:M19384; NID:9189614; PIDN:AAB59545.1; PID:9189615
R/Kaplan, R.; Jave, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.
J. Biol. Chem. 263, 8037-8043, 1988
A/Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+)
A/Reference number: A28076; MUID:88228020; PMID:2967291
A/Accession: A28076
A/Molecule type: mRNA
A/Residues: 1-320 <KAP>
A/Cross-references: GB:J03745; NID:9182111; PIDN:AAA52386.1; PID:9182112
R/Maurer-Pog, I.; Reuteling-Sperger, C.F.M.; Pieters, J.; Bodo, G.; Sira
Eur. J. Biochem. 174, 585-592, 1988
A/Title: Cloning and expression of cDNA for human vascular anticoagulant
A/Reference number: S01016; MUID:88271329; PMID:2455636
A/Accession: S01016
A/Molecule type: mRNA
A/Residues: 1-320 <MAU>
A/Cross-references: EMBL:X12454; NID:937636; PIDN:CAA30965.1; PID:937637
A/Note: part of this sequence was confirmed by protein sequencing
R/Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
Biochemistry 26, 8087-8092, 1987
A/Title: Primary structure of human placental anticoagulant protein.
A/Reference number: A29417; MUID:88163463; PMID:2964863
A/Accession: A29417
A/Molecule type: mRNA
A/Residues: 1-320 <FUN>
A/Cross-references: EMBL:M18366; NID:9179131; PIDN:AAA35570.1; PID:91791
R/Iwasaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saito, Y.; Arai, K.; Mizu
J. Biochem. 102, 1261-1273, 1987
A/Title: Structure and expression of cDNA for an inhibitor of blood coag

A:Reference number: A41514; MUID:88139278; PMID:29638180
A:Accession: A41514
A:Molecule type: mRNA
A:Residues: 1-320 <IWA>
A:Cross-references: GB:D00172; NID:9219480; PIDN:BA00122.1; PID:9219481
A:Note: part of this sequence was confirmed by protein sequencing
R:Schlaepfer, D.D.; Mehlmann, T.; Burgess, W.H.; Haigler, H.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
A:Title: Structural and functional characterization of endonexin II, a calcium- and phospholipid-binding protein
A:Accession: A28038
A:Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
R:Ahm, N.G.; Teller, D.C.; Blenkowski, M.T.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase-A-2 inhibitor.
A:Reference number: A92696; MUID:89066652; PMID:2974032
A:Accession: C31953
A:Molecule type: protein
A:Residues: 85-93 <AHN>
R:Rochhut, B.; Comera, C.; Cortal, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; C. Biochem. J. 263, 929-935, 1989
A:Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with the reference number: S06646; MUID:90088443; PMID:2532007
A:Accession: S06646
A:Molecule type: protein
A:Residues: 7-25, 27-42, 51-74, 'X', 76-151, 181-198, 202-207, 209-226, 228-238, 246-271, 277-282; FEBS Lett. 275, 15-21, 1990
A:Title: The calcium binding sites in human annexin V by crystal structure analysis at 2 A:Reference number: A37250; MUID:91085549; PMID:218156
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
R:Funakoshi, T.; Helmark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K. Biochemistry 26, 5572-5578, 1987
A:Title: Human placental anticoagulant protein: isolation and characterization.
A:Reference number: A29670; MUID:88050845; PMID:2960376
A:Accession: A29670
A:Molecule type: protein
A:Residues: 29-73, 274-297, 300-320 <FU2>
R:Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Careedo, M.T. Gene 149, 253-260, 1994
A:Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C content
A:Reference number: I37172; MUID:95047484; PMID:7958998
A:Accession: I37172
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-320 <RES>
A:Cross-references: EMBL:U01691; NID:9430964; PIDN:AA04047.1; PID:9430966
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid bilipid-binding rather than proteolytic inactivation. It does not affect chromatin-dependent
C:Genetics:
A:Gene: GDB:ANX5
A:Cross-references: GDB:120555; OMIM:131230
A:Map position: 4Q26-4Q28
A:Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F;18-89/Domain: annexin V #status experimental <MAT>
F;18-89/Domain: annexin repeat homology <AX1>
F;29-45/Region: endonexin fold #status predicted
F;90-161/Domain: endonexin repeat homology <AX2>
F;101-117/Region: endonexin fold #status predicted
F;117-245/Domain: annexin repeat homology <AX3>
F;185-201/Region: endonexin fold #status predicted
F;249-320/Domain: annexin repeat homology <AX4>
F;260-276/Region: endonexin fold #status predicted
F;2/Modified site: phosphorylated amino end (Ala) (in mature form) #status experimental
F;2/Binding site: phosphate (Thr) (covalent) #status predicted
F;28,30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental

F;33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental
F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental
F;100,102,104,144/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status experimental
F;259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status experimental
Query Match. 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDIKSE 48
DB 25 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDIKSE 72
RESULT 2
S27214
annexin V - bovine
N:Alternate names: CABP33, CABP37
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C:Accession: S27214; S27215
R:Leamonth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giambanco, I.; B. Biochim. Biophys. Acta 1160, 76-83, 1992
A:Title: Novel isoforms of CABP 33/37 (Annexin V) from mammalian brain: structural and p
A:Reference number: S27214; MUID:93041974; PMID:1420335
A:Accession: S27214
A:Molecule type: protein
A:Residues: 1-320 <LEA>
A:Accession: S27215
A:Molecule type: protein
A:Residues: 1-35, 'T', 37-124, 'E', 126-320 <LE2>
A:Note: It is uncertain whether the sequence differences are due to allelic variation or
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid bilipid-binding rather than proteolytic inactivation. It does not affect chromatin-dependent
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F;17-88/Domain: annexin repeat homology <AX1>
F;28-44/Region: endonexin fold #status predicted
F;89-160/Domain: annexin repeat homology <AX2>
F;100-116/Region: endonexin fold #status predicted
F;172-244/Domain: annexin repeat homology <AX3>
F;184-200/Region: endonexin fold #status predicted
F;248-319/Domain: annexin repeat homology <AX4>
F;259-275/Region: endonexin fold #status predicted
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;32/Binding site: phosphate (Thr) (covalent) #status experimental
F;77,79,31,71/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicted
F;72,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F;72,77/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F;99,101,103,143/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status predicted
F;258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predicted
Query Match. 97.0%; Score 224; DB 1; Length 320;
Best Local Similarity 95.8%; Pred. No. 2.4e-20;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDIKSE 48
DB 24 RKAMKGLTDEESITLTLSRSNAQROEISAFAKTLFGRDLDDIKSE 71
RESULT 3
LUCBS
annexin V - chicken
N:Alternate names: anchorin CIT; endonexin II; lipocortin V; placental anticoagulant prot
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000
C:Accession: A35381; A28623; B40404; S32523; S08771
R:Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfeafle, M.; Deutzmann, R.; Mol J. Biol. Chem. 265, 8344, 1990
A:Reference number: A35381; MUID:90243721; PMID:2159478

A>Status: preliminary
A:Molecule type: protein
A:Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid dectocod.

C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin
F:12-319/Product: annexin IV #status predicted <MAT>
F:17-88/Domain: annexin repeat homology <AX1>
F:28-44/Region: endonexin fold #status predicted
F:89-160/Domain: endonexin repeat homology <AX2>
F:100-116/Region: endonexin fold #status predicted
F:172-244/Domain: annexin repeat homology <AX3>
F:184-200/Region: endonexin repeat homology <AX4>
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin repeat homology <AX4>
F:7/Binding site: phosphate (Thr) (covalent) #status predicted
F:125,245/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 74.9%; Score 173; DB 1; Length 319;
Best Local Similarity 70.8%; Pred. No. 5.7e-14;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 1 RKAMKGLTDEESITLTLTSRSMQROEISAFTLFGRLDLDLKDSE 48
Db 24 RKAMKGLTDEDAITVLAIVYSTRQROEIRAYKTTTGRDLDLKDSE 71

RESULT 6

annexin IV - pig
N:Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1999
C:Accession: A27107
R:Weber, K.; Johnson, N.; Pleesmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekerckh
EMBO J. 6, 1599-1604, 1987
A:Title: The amino acid sequence of protein II and its phosphorylation site for protein
A:Reference number: A27107; MUID:87257850; PMID:2956093
A:Accession: A27107
A:Molecule type: protein
A:Residues: 1-318 <MEB>
A:Experimental source: intestinal epithelium
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid dectocod.

C:Superfamily: annexin I; annexin repeat homology
C:Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:171-243/Region: endonexin repeat homology <AX3>
F:199-115/Region: endonexin repeat homology <AX3>
F:183-199/Region: endonexin repeat homology <AX3>
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: annexin repeat homology <AX4>
F:6/Modified site: phosphate (Thr) (covalent) (probably acetylated) #status experimental
F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:124,244/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 74.5%; Score 172; DB 1; Length 318;
Best Local Similarity 70.8%; Pred. No. 7.6e-14;
Matches 34; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Oy 1 RKAMKGLTDEESITLTLTSRSMQROEISAFTLFGRLDLDLKDSE 48
Db 23 RKAMKGLTDEDAITVLAIVYSTRQROEIRAYKTTTGRDLDLKDSE 70

RESULT 7

annexin VII - mouse
N:Alternate names: synexin
C:Species: Mus musculus (house mouse)

C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 13-Aug-1999
C:Accession: S29170; S46209; S51173
R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
Biochem. J. 289, 735-741, 1993
A:Title: Mouse synexin (annexin VII) polymorphisms and a phylogenetic comparison with oti
A:Reference number: S29170; MUID:93168121; PMID:7916616
A:Accession: S29170
A:Molecule type: mRNA
A:Residues: 1-463 <ZHA>
A:Cross-references: EMBL:L13129

R:Zhang-Keck, Z.Y.; Stivastava, M.; Kozak, C.A.; Caohuy, H.; Shirvan, A.; Burns, A.L.; P
Biochem. J. 301, 835-845, 1994
A:Title: Genomic organization and chromosomal localization of the mouse synexin gene.
A:Reference number: S46209; MUID:94330961; PMID:8053905
A:Accession: S46209
A:Molecule type: DNA
A:Residues: 1-463 <ZHF>
R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.
submitted to the EMBL Data Library, May 1993
A:Reference number: S51173
A:Accession: S51173
A:Molecule type: mRNA
A:Residues: 1-144,'S',146-303,'A',305-463 <ZHW>
A:Cross-references: EMBL:L13129; NID:9293293; PIDN:AA37238.1; PID:9293294
A:Gene: MGI:Anx7

A:Map position: 14
A:Insertions: 19/3; 87/1; 121/1; 142/3; 177/1; 208/3; 246/3; 303/3; 360/3; 386/1; 423/3
C:Superfamily: annexin VII; annexin repeat homology
C:Keywords: calcium channel; ion channel
F:163-234/Domain: annexin repeat homology <AX1>
F:235-306/Domain: annexin repeat homology <AX2>
F:318-390/Domain: annexin repeat homology <AX3>
F:394-463/Domain: annexin repeat homology <AX4>

Query Match 73.2%; Score 169; DB 2; Length 463;
Best Local Similarity 64.6%; Pred. No. 2.7e-13;
Matches 31; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Oy 1 RKAMKGLTDEESITLTLTSRSMQROEISAFTLFGRLDLDLKDSE 48
Db 170 RKAMKGLTDEDAITVLAIVYSTRQROEIRAYKTTTGRDLDLKDSE 217

RESULT 8

annexin IV - human
N:Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
C:Species: Homo sapiens (man)
C:Date: 30-Jan-1993 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: A42077; B42077; S07434; A31953; A31046
R:Rat, J.F.; Smith, C.; Frankberry, D.A.; Miao, C.H.; Adler, D.A.; Distche, C.M.
Genomics 12, 313-318, 1992
A:Title: Chromosomal mapping of the human annexin IV (ANX4) gene.
A:Reference number: A42077; MUID:92155721; PMID:1346776
A:Accession: A42077
A:Molecule type: mRNA
A:Residues: 1-321 <TAI>
A:Cross-references: GB:M82809; NID:9178698; PIDN:AAA51740.1; PID:9178699
A:Accession: B42077
A:Molecule type: DNA
A:Residues: 87-129 <TA2>
R:Grundmann, U.; Amann, E.; Abel, K.J.; Kuepper, H.A.
Behring Inst. Mitt. 82, 59-67, 1988
A:Title: Isolation and expression of cDNA coding for a new member of the phospholipase A:
A:Reference number: S07434; MUID:88309022; PMID:2970257
A:Accession: S07434
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97,'Q',99-321 <GRU>
A:Cross-references: EMBL:M9383; NID:9189616; PIDN:AA41689.1; PID:9189617
R:Ahm, N.G.; Teller, D.C.; Blenkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.

J. Biol. Chem. 263, 18657-18663, 1988.
A>Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2
ibitor.
A/Reference number: A92696; PMID:8906652; PMID:2974032
A/Accession: A31953
A/Molecule type: protein
A/Residues: 29-58;101-126;282-310 <AAN>
R/Tait, J.F.; Sakata, M.; McMullen, B.A.; Mao, C.H.; Funakoshi, T.; Hendrickson, L.E.;
Biochemistry 27, 6268-6276, 1988
A>Title: Placental anticoagulant proteins: isolation and comparative characterization of
A/Reference number: A90534; PMID:89118212; PMID:2975506
A/Accession: A31046
A/Molecule type: protein
A/Residues: 4-17;30-74;102-146;283-321 <TA3>
C/Genetics:
A/Gene: GDB:ANX4
A/Cross-references: GDB:131395; OMIM:106491
A/Map position: 2p13-2p13
A/Introns: 102/3
C/Superfamily: annexin I; annexin repeat homology
C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; glycopro
F/2-321/Product: annexin IV #status predicted <MAT>
F/19-90/Domain: annexin repeat homology <AX1>
F/30-46/Region: endonexin fold #status predicted
F/91-162/Domain: annexin repeat homology <AX2>
F/102-118/Region: endonexin fold #status predicted
F/174-246/Domain: annexin repeat homology <AX3>
F/186-202/Region: endonexin fold #status predicted
F/250-321/Domain: annexin repeat homology <AX4>
F/261-277/Region: endonexin fold #status predicted
F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F/9/Binding site: phosphate (Thr) (covalent) #status predicted
F/247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.3%; Score 167; DB 1; Length 321;
Best Local Similarity 66.7%; Pred. No. 3.2e-13;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTSRNSNAQROEISAFKTLFGRLDLDLXSE 48
DB 26 RKAMKGLTDEDAITISVLAIRNNAQROEIRYAKSTIGRLDLDLXSE 73

RESULT 9
AQUH68
annexin VI [validated] - human
N/Alternate names: calcium-binding protein, 68k, calelectrin, calphobindin II
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text change 08-Dec-2000
C/Accession: J00032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507
R/Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh
J. Biochem. 106, 43-49, 1988
A>Title: Structure and expression of cDNA for calphobindin II, a human placental coagula
A/Reference number: J00032; PMID:89380132; PMID:2528541
A/Accession: J00032
A/Molecule type: mRNA
A/Residues: 1-673 <IWA>
A/Cross-references: EMBL:D00510; NID:9219550; PIDD:BA00400.1; PIDD:9219551
R/Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crompton, M.J.
EMBO J. 7, 21-27, 1988
A>Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68;
A/Reference number: S00263; PMID:88196081; PMID:3258820
A/Accession: S00263
A/Molecule type: mRNA
A/Residues: 1-618; 'D', 620-673 <CR1>
A/Cross-references: EMBL:X00097; NID:935217; PIDD:CAA68286.1; PIDD:935218
A/Accession: S18519
A/Molecule type: protein
A/Residues: 103-113;167-172, 'X', 174-177;232-235, 'F', 237-240;251-258;277-281;359-362, 'G',
A/Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu
A/Note: eight calcium ions are bound in the presence of phospholipid
R/Stedhof, T.C.; Slaughter, C.A.; Leznicki, I.; Barton, P.; Reynolds, G.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988

A>Title: Human 67-kDa calelectrin contains a duplication of four repeats f
A/Reference number: A31079; PMID:88124902; PMID:2963335
A/Accession: A31079
A/Molecule type: mRNA
A/Residues: 1-225; 'MK', 228-554, 'T', 556-673 <SUE>
A/Cross-references: GB:J03578; NID:9179975; PIDD:AAA5656.1; PIDD:9179976
R/Ishizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Ma
J. Biochem. 107, 43-50, 1980
A>Title: Structure and properties of calphobindin II, an
A/Reference number: JX0091; PMID:90236978; PMID:2139657
A/Accession: JX0091
A/Molecule type: protein
A/Residues: 2-299;307-314;320-445;447-549;581-673 <YOS>
R/Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakumaga, T.
J. Biol. Chem. 264, 17222-17230, 1989
A>Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-
A/Reference number: A34459; PMID:9008880; PMID:2529258
A/Accession: B34459
A/Molecule type: protein
A/Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>
A/Experimental source: Placenta
R/Alm, N.G.; Jeller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.
J. Biol. Chem. 263, 18657-18663, 1988
A>Title: Sedimentation equilibrium analysis of five lipocortin-related ph
ibitor.
A/Reference number: A92696; PMID:8906652; PMID:2974032
A/Accession: B31953
A/Molecule type: protein
A/Residues: 90-108; 'L', 110-126;127, 265-276;286-302;626-654 <AAN>
R/Hytt, S.L.; Liao, L.; Chapline, C.; Jaken, S.
Biochemistry 33, 1223-1228, 1994
A>Title: Identification and characterization of alpha-protein kinase C b
A/Reference number: A53507; PMID:94153907; PMID:8110754
A/Accession: A53507
A/Molecule type: protein
A/Residues: 'X', 473-480, 'DY', <HYA>
A/Comment: This abundant cytosolic protein binds to the inner surface of
C/Genetics:
A/Gene: GDB:ANX6
A/Cross-references: GDB:119681; OMIM:114070
A/Map position: 5q32-5q34
C/Superfamily: annexin VI; annexin repeat homology
C/Keywords: acetylated amino end; calcium binding; duplication; endonexin
F/2-673/Product: annexin VI #status experimental <MAT>
F/23-94/Domain: annexin repeat homology <AX1>
F/34-50/Region: endonexin fold #status predicted
F/95-166/Domain: annexin repeat homology <AX2>
F/106-122/Region: endonexin fold #status predicted
F/178-250/Domain: annexin repeat homology <AX3>
F/190-206/Region: endonexin fold #status predicted
F/224-325/Domain: annexin repeat homology <AX4>
F/265-281/Region: endonexin fold #status predicted
F/366-437/Domain: annexin repeat homology <AX5>
F/373-393/Region: endonexin fold #status predicted
F/438-509/Domain: annexin repeat homology <AX6>
F/449-465/Region: endonexin fold #status predicted
F/457-588/Domain: annexin repeat homology <AX7>
F/538-554/Region: endonexin repeat homology <AX8>
F/602-673/Domain: annexin repeat homology <AX9>
F/613-659/Region: endonexin fold #status predicted
F/2/Modified site: acetylated amino end (Ala) (in mature form) #status e

Query Match 72.3%; Score 167; DB 1; Length 673;
Best Local Similarity 66.7%; Pred. No. 7.4e-13;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESILTLTSRNSNAQROEISAFKTLFGRLDLDLXSE 48
DB 373 RKAMKGLTDEDDITLITHTSNVQROEIRQTFKSHFGRLDLDLXSE 420

RESULT 10
S09020

calcinmedin, 32K - chicken (fragments)
C/Species: Gallus gallus (chicken)
C/Date: 21-Nov-1993 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C/Accession: S09020
R/Kobayashi, R.; Hidaka, H.; Tashima, Y.
Arch. Biochem. Biophys. 277, 203-210, 1990
A/Title: Purification, characterization, and partial sequence analysis of 32-kDa calcine
A/Reference number: S09020; MUID:90165469; PMID:2137684
A/Accession: S09020
A/Molecule type: protein
A/Residues: 1-36;37-53;54-64;65-81;82-105;106-116;117-137;138-150;151-157 <ROB>
C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid
derespoor.

C/Superfamily: annexin I; annexin repeat homology
C/Keywords: blocked amino end; calcium binding; collagen binding; duplication; endonexin
F/15-36/Domain: annexin repeat homology (fragment) <AX1A>
F/37-53/Domain: annexin repeat homology (fragment) <AX1B>
F/54-64/Domain: annexin repeat homology (fragment) <AX1C>
F/65-71/Domain: annexin repeat homology (fragment) <AX2A>
F/72-102/Domain: annexin repeat homology (fragment) <AX2B>
F/103-116/Domain: annexin repeat homology (fragment) <AX3A>
F/117-137/Domain: annexin repeat homology (fragment) <AX3B>
F/138-150/Domain: annexin repeat homology (fragment) <AX3C>
F/30,32,33/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted

Query Match
Best Local Similarity 71.9%; Score 166; DB 2; Length 157;
Matches 36; Conservative 6; Mismatches 1; Indels 2; Gaps 2;

OY 1 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 45
Db 22 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 64

RESULT 11
JC2029

N/Alternate names: 67K lipid-dependent Ca²⁺-binding protein
C/Species: Gallus gallus (chicken)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C/Accession: JC2029
R/Cao, X.; Geng, B.R.; Wu, L.N.Y.; Buzzi, W.R.; Showman, R.M.; Wuthier, R.E.
Biochem. Biophys. Res. Commun. 197, 556-561, 1993
A/Title: Characterization, cloning and expression of the 67-kDa annexin from chicken gero
A/Reference number: JC2029; MUID:94092130; PMID:8267550
A/Accession: JC2029
A/Molecule type: mRNA
A/Residues: 1-671 <CAO>
C/Superfamily: annexin VI; annexin repeat homology
C/Keywords: calcium binding; phospholipid binding
F/21-92/Domain: annexin repeat homology <AX1>
F/93-164/Domain: annexin repeat homology <AX2>
F/176-248/Domain: annexin repeat homology <AX3>
F/252-323/Domain: annexin repeat homology <AX4>
F/364-435/Domain: annexin repeat homology <AX5>
F/436-507/Domain: annexin repeat homology <AX6>
F/525-597/Domain: annexin repeat homology <AX7>
F/601-671/Domain: annexin repeat homology <AX8>

Query Match
Best Local Similarity 71.9%; Score 166; DB 2; Length 671;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 48
Db 371 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 418

RESULT 12
S01786

N/Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: S01786
R/Moss, S.E.; Crompton, M.R.; Crompton, M.J.
Eur. J. Biochem. 177, 21-27, 1989
A/Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family
A/Reference number: S01786; MUID:89030687; PMID:2972541
A/Accession: S01786
A/Molecule type: mRNA
A/Residues: 1-673 <MOSS>

A/Cross-references: EMBL:X13460; NID:953580; PIDN:CAA31808.1; PID:953581
C/Comment: This abundant cytosolic protein binds to the inner surface of the cell membrane
C/Superfamily: annexin VI; annexin repeat homology
F/2-673/Product: annexin VI #status predicted
F/23-94/Domain: annexin repeat homology <AX1>
F/95-166/Domain: annexin repeat homology <AX2>
F/106-122/Domain: annexin repeat homology <AX3>
F/178-250/Domain: annexin repeat homology <AX4>
F/190-206/Domain: annexin repeat homology <AX5>
F/254-325/Domain: annexin repeat homology <AX6>
F/326-437/Domain: annexin repeat homology <AX7>
F/438-509/Domain: annexin repeat homology <AX8>
F/449-465/Region: endonexin fold #status predicted
F/527-598/Domain: annexin repeat homology <AX7>
F/538-554/Region: endonexin fold #status predicted
F/602-673/Domain: annexin repeat homology <AX8>
F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match
Best Local Similarity 71.0%; Score 164; DB 1; Length 673;
Matches 32; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 48
Db 373 RKAMKGLGTDEESITLTLSRSNAOROEISAAPFTLFRDLDDL 420

RESULT 13
L0H07

N/Alternate names: annexin VII, long form - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1992 #sequence_revision 26-Jan-1996 #text_change 22-Jun-1999
C/Accession: A54467; A32554; A39513; B39513
R/Shivan, A.; Srivastava, M.; Wang, M.G.; Cultraro, C.; Magendzo, K.; McBride, O.W.; Pol
Biochemistry 33, 6888-6901, 1994
A/Title: Divergent structure of the human synexin (annexin VII) gene and assignment to cl
A/Reference number: A54467; MUID:94264005; PMID:7515686
A/Accession: A54467
A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA
A/Residues: 1-488 <SHI>
R/Burns, A.L.; Magendzo, K.; Shivan, A.; Srivastava, M.; Rojas, E.; Aljani, M.R.; Polle
Proc. Natl. Acad. Sci. U.S.A. 86, 3798-3802, 1989
A/Title: Calcium channel activity of purified human synexin and structure of the human sy
A/Reference number: A32554; MUID:89264510; PMID:2542947
A/Accession: A32554
A/Molecule type: mRNA

A/Cross-references: EMBL:J04543; NID:9338243; PIDN:AAA3616.1; PID:9338244
R/Magendzo, K.; Shivan, A.; Cultraro, C.; Srivastava, M.; Pollard, H.B.; Burns, A.L.
J. Biol. Chem. 266, 3228-3232, 1991
A/Title: Alternative splicing of human synexin mRNA in brain, cardiac, and skeletal muscle
A/Reference number: A39513; MUID:91131630; PMID:1825209
A/Accession: A39513
A/Molecule type: mRNA
A/Residues: 137-145, 168-176 <MAG>

A:Cross-references: EMBL:J05732
 A:Accession: B39513
 A:Molecule type: mRNA
 A:Residues: 137-176 <MA2>
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid.
 C:Comment: The long form of annexin VII is more prevalent in brain, heart, and skeletal muscle.
 C:Genetics:
 A:Gene: GDB:ANX7
 A:Cross-references: GDB:369042; OMIM:186360
 A:Map position: 10q21.1-10q21.2
 A:Introns: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1; 44
 C:Superfamily: annexin VII; annexin repeat homology
 C:Keywords: alternative splicing; calcium binding; calcium channel; duplication; endonex
 F:1-488/Product: annexin VII, long form #status predicted <MA2>
 F:1-145,168-488/Product: annexin VII, short form #status predicted <MA3>
 F:188-259/Domain: annexin repeat homology <AX1>
 F:189-215/Region: endonexin fold #status predicted
 F:260-331/Domain: annexin repeat homology <AX2>
 F:271-287/Region: endonexin fold #status predicted
 F:343-415/Domain: annexin repeat homology <AX3>
 F:355-371/Region: endonexin fold #status predicted
 F:419-488/Domain: annexin repeat homology <AX4>
 F:430-446/Region: endonexin fold #status predicted

Query Match 70.6%; Score 163; DB 1; Length 488;
 Best Local Similarity 64.6%; Pred. No. 1.6e-12;
 Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDESIITLTSRSNAORQISAFKTLFGRLDLDLXSE 48
 Db 195 RKAMKGTDEQAIIVDVANRSNDQKIKAFKTSYKDLIDLXSE 242

RESULT 14

S52844

annexin VI - rat

N:Alternate names: calcium-binding protein 65/67

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S65683; S52844

C:Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.

Eur. J. Biochem. 230, 741-751, 1995

A:Title: CDNA cloning and tissue-specific regulation of expression of rat calcium-binding

A:Reference number: S65683; MUID:95331313; PMID:7607247

A:Accession: S65683

A:Molecule type: mRNA

A:Residues: 1-673 <FAN>

A:Cross-references: EMBL:X86086; NID:9763180; PIDD:CA60040.1; PID:9763181

A:Experimental source: liver

C:Superfamily: annexin VI; annexin repeat homology

C:Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associated P

F:2-673/Product: annexin VI #status predicted <MAT>

F:23-94/Domain: annexin repeat homology <AX1>

F:34-50/Region: endonexin fold #status predicted

F:99-166/Domain: annexin repeat homology <AX2>

F:106-122/Region: endonexin fold #status predicted

F:178-250/Domain: annexin repeat homology <AX3>

F:180-206/Region: endonexin fold #status predicted

F:254-325/Domain: annexin repeat homology <AX4>

F:265-281/Region: endonexin fold #status predicted

F:366-437/Domain: annexin repeat homology <AX5>

F:377-393/Region: endonexin fold #status predicted

F:438-509/Domain: annexin repeat homology <AX6>

F:449-465/Region: endonexin fold #status predicted

F:527-598/Domain: annexin repeat homology <AX7>

F:538-554/Region: endonexin fold #status predicted

F:602-673/Domain: annexin repeat homology <AX8>

F:613-629/Region: endonexin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match

Best Local Similarity 70.1%; Score 162; DB 1; Length 673;

64.6%; Pred. No. 3.1e-12;

Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps

QY 1 RKAMKGLGTDESIITLTSRSNAORQISAFKTLFGRLDLDLXSE 48
 Db 373 RKAMKGTDEQAIIVDVANRSNDQKIKAFKTSYKDLIDLXSE 420

RESULT 15

LUBO11

annexin XI form A - bovine

N:Alternate names: calyculin-associated protein peptide, CAP-50

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C:Accession: A42113; A42909; B42909; C42909; D42909

R:Rowle, C.A.; Treadwell, B.V.

J. Biol. Chem. 267, 5416-5423, 1992

A:Title: Identification of a novel mammalian annexin. cDNA cloning, sequen

A:Reference number: A42113; MUID:92184796; PMID:1372001

A:Accession: A42113

A:Molecule type: mRNA

A:Residues: 1-503 <TOM>

A:Cross-references: GB:M82802; NID:9162673; PIDD:AAA0379.1; PID:9162674

A:Note: the authors did not translate the codon GAC for residue 503

R:Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi

J. Biol. Chem. 267, 13498-13504, 1992

A:Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured

A:Reference number: A42909; MUID:92317074; PMID:1618851

A:Accession: A42909

A:Molecule type: protein

A:Residues: 213-223, 'X', 225-226, 319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-336

A:Experimental source: lung

A:Note: sequence modified after extraction from NCBI backbone

C:Comment: Annexins undergo reversible, calcium-dependent binding to membr

derstood.

C:Genetics:

A:Introns: 19/1; 56/2

A:Note: the list of introns is incomplete

C:Superfamily: annexin VII; annexin repeat homology

C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; p

F:201-272/Domain: annexin repeat homology <AX1>

F:212-228/Region: endonexin fold #status predicted

F:273-344/Domain: annexin repeat homology <AX2>

F:284-300/Region: endonexin fold #status predicted

F:366-428/Domain: annexin repeat homology <AX3>

F:368-384/Region: endonexin fold #status predicted

F:432-503/Domain: annexin repeat homology <AX4>

F:443-459/Region: endonexin fold #status predicted

F:59,111/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.8%; Score 159; DB 1; Length 503;
 Best Local Similarity 64.6%; Pred. No. 5.3e-12;

Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps

QY 1 RKAMKGLGTDESIITLTSRSNAORQISAFKTLFGRLDLDLXSE 48
 Db 208 RKAMKGTDEQAIIVDVANRSNDQKIKAFKTSYKDLIDLXSE 255

Search completed: April 8, 2004, 11:58:39
 Job time : 21 sec

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Thu Apr 8 13:28:54 2004

us-09-787-923-2_copy_25_72.apr082004.ra1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:55:51 ; Search time 23 Seconds
(without alignments)
107.741 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72

Perfect score: 231
Sequence: 1 RKMKGGLGDEESILTLTFS.....ISNAFKTLRGLDLDKSE 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6CTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	231	100.0	319	1	US-08-125-746-1 Sequence 1, Appli
2	231	100.0	320	1	US-08-125-746-3 Sequence 3, Appli
3	231	100.0	320	4	US-08-948-276-1 Sequence 1, Appli
4	231	100.0	320	6	US-08-948-276-1 Patent No. 5225537
5	231	100.0	327	4	US-09-324-096A-2 Sequence 2, Appli
6	231	100.0	327	4	US-09-324-096A-4 Sequence 6, Appli
7	231	100.0	327	4	US-09-324-096A-6 Sequence 2, Appli
8	207	89.6	319	4	US-08-948-276-2 Sequence 3, Appli
9	194	84.0	319	2	US-08-948-276-3 Sequence 2, Appli
10	194	84.0	319	2	US-08-149-975A-2 Sequence 14, Appli
11	173	74.9	319	3	US-08-526-136-14 Sequence 4, Appli
12	167	72.3	321	4	US-08-948-276-4 Sequence 13, Appli
13	163	70.6	466	3	US-08-526-136-13 Sequence 2, Appli
14	159	68.8	503	3	US-08-526-136-2 Sequence 5, Appli
15	159	68.8	503	3	US-08-526-136-4 Sequence 16, Appli
16	131	56.7	323	4	US-09-010-147B-16 Sequence 6, Appli
17	110	47.6	324	4	US-08-948-276-5 Sequence 39, Appli
18	108	46.8	346	4	US-09-325-832A-66 Sequence 65, Appli
19	98	42.4	184	4	US-09-325-832A-65 Sequence 62, Appli
20	88	38.1	239	4	US-09-325-832A-62 Sequence 747, App
21	82	35.5	316	4	US-09-732-210-747 Sequence 220, App
22	63.5	27.5	93	4	US-09-634-238-220 Sequence 2, Appli
23	55.5	24.0	234	3	US-08-736-915-2 Sequence 24, Appli
24	54.5	23.6	2318	4	US-09-091-219-24 Sequence 24, Appli
25	54.5	23.6	2318	4	US-09-660-541-24 Sequence 24, Appli
26	54.5	23.6	2318	4	US-09-660-541-24 Sequence 24, Appli
27	54.5	23.6	2318	4	US-09-660-541-24 Sequence 24, Appli

28	53.5	23.2	297	4	US-09-543-681A-6240
29	53.5	23.2	450	4	US-09-489-039A-13998
30	53.5	23.2	608	4	US-08-843-572E-2
31	53	22.9	1996	2	US-08-804-227C-9
32	53	22.9	1996	2	US-08-804-198-3
33	53	22.9	4445	2	US-08-804-227C-14
34	53	22.9	4450	2	US-08-804-227C-8
35	53	22.9	4550	2	US-08-804-198-2
36	52.5	22.7	392	4	US-09-489-039A-9827
37	52	22.5	151	4	US-09-621-976-4980
38	52	22.5	410	4	US-09-594-506-34
39	52	22.5	433	4	US-09-489-039A-8953
40	52	22.5	1037	4	US-09-543-681A-7677
41	52	22.5	1398	4	US-09-543-681A-5641
42	52	22.5	3788	4	US-09-336-447A-76
43	51.5	22.3	342	4	US-09-107-532A-5664
44	51	22.1	675	4	US-09-591-095-8
45	51	22.1	819	4	US-09-328-352-5342

ALIGNMENTS

RESULT 1
US-08-125-746-1
Sequence 1, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08125746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 18428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAI UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein

Sequence 6240,
Sequence 13998
Sequence 2, Ap
Sequence 9, Ap
Sequence 3, Ap
Sequence 14, A
Sequence 8, Ap
Sequence 9827,
Sequence 4980,
Sequence 34, A
Sequence 7677
Sequence 5641
Sequence 76, A
Sequence 5664
Sequence 8, Ap
Sequence 5342

US-08-125-746-1

Query Match 100.0%; Score 231; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 48
DB 24 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 71

RESULT 2

US-08-125-746-3
Sequence 3, Application US/08125746
Patent No. 5591633

GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: IWASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-125-746-3

Query Match 100.0%; Score 231; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 3

US-08-948-276-1

Sequence 1, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:

APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: US97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: human
US-08-948-276-1

Query Match 100.0%; Score 231; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 4

522537-4

APPLICANT: ROSTER, DONALD
TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/459,082
FILING DATE: 29-DEC-1989
SEQ ID NO:4
LENGTH: 320
522537-4

Query Match 100.0%; Score 231; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 5

US-09-324-096A-2

Sequence 2, Application US/09324096A
Patent No. 6323313
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOEW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-324-096A-2

Query Match 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESILTLTSSRNAQROEISAFAKTLFGRLDLDLXSE 48

Thu Apr 8 13:28:54 2004

us-09-787-923-2_copy_25_72.apr082004.ra1

Db 32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 79

RESULT 6
US-09-324-096A-4
; Sequence 4, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOPW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-4

Query Match
Best Local Similarity 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 48
32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 79

RESULT 7
US-09-324-096A-6
; Sequence 6, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOPW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-6

Query Match
Best Local Similarity 100.0%; Score 231; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 48
32 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 79

RESULT 8
US-08-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2

LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
US-08-948-276-2

Query Match
Best Local Similarity 89.6%; Score 207; DB 4; Length 319;
Best Local Similarity 87.5%; Pred. No. 1.5e-22;
Matches 42; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 48
23 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 70

RESULT 9
US-08-948-276-3
; Sequence 3, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 318
; TYPE: PRT
; ORGANISM: rat
US-08-948-276-3

Query Match
Best Local Similarity 84.0%; Score 194; DB 4; Length 318;
Best Local Similarity 79.2%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 48
22 RKAMKGLGTDEESITLTLTSSNAQROEISAFAFKTLFGRLDLDLXSE 69

RESULT 10
US-08-149-975A-2
; Sequence 2, Application US/08149975A
; Patent No. 5849600
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; APPLICANT: Honda, Yoshiyuki
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-149-975A-2

Query Match 84.0%; Score 194; DB 2; Length 319;
Best Local Similarity 79.2%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESITLTLSRNSAQRQEIISAFKTLFGDLDLDDKSE 48
23 RKAMKGLTDEESITLTLSRNSAQRQEIISAFKTLFGDLDLDDKSE 70

RESULT 11
US-08-526-136-14
Sequence 14, Application US/08526136
Patent No. 6107089

GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 319
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-526-136-14

Query Match

Best Local Similarity 74.9%; Score 173; DB 3; Length 319;
Matches 34; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESITLTLSRNSAQRQEIISAFKTLFGDLDLDDKSE 48

Db 24 RKAMKGLTDEDAIINVLAYSTAQRQEIIRTAVKTTIGRDLDMDLCKSE 71

RESULT 12
US-08-948-276-4

Sequence 4, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: USCF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 321
TYPE: PRT
ORGANISM: human
US-08-948-276-4

Query Match 72.3%; Score 167; DB 4; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.3e-16;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 RKAMKGLTDEESITLTLSRNSAQRQEIISAFKTLFGDLDLDDKSE 48
26 RKAMKGLTDEDAIINVLAYSTAQRQEIIRTAVKTTIGRDLDMDLCKSE 73

RESULT 13
US-08-526-136-13

Sequence 13, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 466
TYPE: amino acid

Thu Apr 8 13:28:54 2004

us-09-787-923-2_copy_25_72.apr082004.ra1

Page

STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-526-136-13

Query Match 70.6%; Score 163; DB 3; Length 466;
Best Local Similarity 64.6%; Pred. No. 8.2e-16;
Matches 31; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 RRAMKGLGTDESSITLTLTSRNSAORQISAAFKTLFGRLDDKSE 48
DB 173 RRAMKGFGTDEQAIIVDVANRSNDQOKIKAAFKTSYGKDLIKDLSKSE 220

RESULT 14
US-08-526-136-2
Sequence 2, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-2

Query Match 68.8%; Score 159; DB 3; Length 503;
Best Local Similarity 64.6%; Pred. No. 3.5e-15;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRAMKGLGTDESSITLTLTSRNSAORQISAAFKTLFGRLDDKSE 48
DB 208 RRAMKGFGTDEQAIIDCLGRSNKQROQILSFKTA YGKDLIKDLSKSE 255

RESULT 15
US-08-526-136-4
Sequence 4, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:

APPLICANT: Towle, Christine A. et al.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match 68.8%; Score 159; DB 3; Length 505;
Best Local Similarity 64.6%; Pred. No. 3.6e-15;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 RRAMKGLGTDESSITLTLTSRNSAORQISAAFKTLFGRLDDKSE 48
DB 210 RRAMKGFGTDEQAIIDCLGRSNKQROQILSFKTA YGKDLIKDLSKSE 257

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Job time: 23 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:56:56 ; Search time 40 Seconds
(without alignments)
315.526 Million cell updates/sec

Title: US-09-787-923-2_COPY_25_72
Perfect score: 231
Sequence: 1 RKAMKGLTDEESITLTLSR...ISAFKTLFGRLDLDLKS 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 segs, 262937947 residues 1073127

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	231	100.0	320 13 US-10-007-761-72	Sequence 72, App
3	231	100.0	320 16 US-10-424-232-1	Sequence 1, Appli
4	231	100.0	327 9 US-09-970-969-2	Sequence 2, Appli
5	231	100.0	327 9 US-09-970-969-4	Sequence 4, Appli
6	231	100.0	327 9 US-09-970-969-6	Sequence 6, Appli
7	194	84.0	319 14 US-10-080-370-3	Sequence 3, Appli
8	194	84.0	669 14 US-10-080-370-6	Sequence 6, Appli
9	167	72.3	321 14 US-10-097-340-10	Sequence 10, Appl
10	167	72.3	324 9 US-09-925-301-1062	Sequence 1062, Ap
11	167	72.3	675 12 US-10-114-270-160	Sequence 160, Ap
12	163	70.6	485 9 US-09-925-300-1664	Sequence 1664, Ap
13	150	64.9	327 15 US-10-236-031B-18	Sequence 18, Appl
14	133	57.6	158 9 US-09-925-297-479	Sequence 479, App
15	131	56.7	323 14 US-10-205-823-34	Sequence 34, Appl

16	128	55.4	173 12 US-10-424-599-203868	Sequence 2038
17	124	53.7	324 14 US-10-316-253-262	Sequence 262,
18	119	51.5	346 14 US-10-316-253-300	Sequence 300,
19	111	48.1	289 9 US-09-925-301-897	Sequence 897,
20	111	48.1	339 9 US-09-974-298-91	Sequence 91, A
21	111	48.1	339 9 US-10-097-340-6	Sequence 6, A
22	111	48.1	339 14 US-10-097-340-8	Sequence 8, A
23	109	47.2	181 15 US-10-104-047-2800	Sequence 2800
24	109	47.2	327 9 US-09-764-853-615	Sequence 615,
25	109	47.2	332 10 US-09-764-881-110	Sequence 110,
26	109	47.2	332 15 US-10-242-747-110	Sequence 110,
27	108	46.8	319 14 US-10-304-287-2	Sequence 2, A
28	108	46.8	346 9 US-09-919-172-39	Sequence 39, A
29	108	46.8	346 9 US-09-974-298-93	Sequence 93, A
30	108	46.8	373 9 US-09-925-301-888	Sequence 888,
31	108	46.8	388 12 US-10-276-774-2250	Sequence 2250
32	107	46.3	82 9 US-09-925-301-1467	Sequence 1467,
33	103	44.6	319 12 US-10-424-599-213299	Sequence 213299
34	102	44.2	314 12 US-10-424-599-279847	Sequence 279847
35	102	44.2	324 12 US-10-425-114-43962	Sequence 43962
36	100	43.3	320 12 US-10-424-599-201908	Sequence 201908
37	99	42.9	304 12 US-10-424-599-231427	Sequence 231427
38	99	42.9	449 15 US-10-369-493-12408	Sequence 12408
39	98	42.4	107 12 US-10-424-599-279848	Sequence 279848
40	98	42.4	184 14 US-10-219-220-66	Sequence 66,
41	98	42.4	184 15 US-10-393-840-52	Sequence 52,
42	98	42.4	184 15 US-10-393-840-118	Sequence 118
43	98	42.4	313 12 US-10-424-599-279849	Sequence 279849
44	98	42.4	320 12 US-10-425-114-55270	Sequence 55270
45	98	42.4	518 15 US-10-369-493-3240	Sequence 3240

ALIGNMENTS

RESULT 1
US-09-925-302-731
Sequence 731, Application US/09925302
Patent No. US200204941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925.302
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 731
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-731

Query Match 100.0%; Score 231; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB 28 RKAMKGLTDEESITLTLSR...ISAFKTLFGRLDLDLKS 75
1 RKAMKGLTDEESITLTLSR...ISAFKTLFGRLDLDLKS 48
Sequence 72, Application US/10007761
Publicat No. US20020150984A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Peptides for Activation and Inhibition

TITLE OF INVENTION: of delta-PKC
FILE REFERENCE: S8600-8208.US00
CURRENT APPLICATION NUMBER: US/10/007,761
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/262,060
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-761-72

Query Match 100.0%; Score 231; DB 13; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 25 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 3
US-10-424-232-1
Sequence 1, Application US/10424232.
Publication No. US20040022731A1
GENERAL INFORMATION:
APPLICANT: Bogdanov, Alexei
APPLICANT: Schellenberger, Eyk
APPLICANT: Petrovsky, Alexander
APPLICANT: Josephson, Lee
TITLE OF INVENTION: In vivo Imaging of Apoptosis
FILE REFERENCE: 00786-549001
CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/60/376,052
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-424-232-1

Query Match 100.0%; Score 231; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 25 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 72

RESULT 4
US-09-970-969-2
Sequence 2, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-2

Query Match 100.0%; Score 231; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 48
DB 32 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 5
US-09-970-969-4
Sequence 4, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-4

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Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 6
US-09-970-969-6
Sequence 6, Application US/09970969
Patent No. US20020103341A1
GENERAL INFORMATION:
APPLICANT: Tait, Jonathan F.
APPLICANT: Brown, David S.
TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
FILE REFERENCE: uofw-1-13841
CURRENT APPLICATION NUMBER: US/09/970,969
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-970-969-6

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Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 RKAMKGLGDEESITLTLSRSNAQROEISAFAKTLFGRLDLDLXSE 79

RESULT 7
US-10-080-370-3
Sequence 3, Application US/10080370
Publication No. US2003016532A1
GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis


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FILE REFERENCE: SURR.30
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,582
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-080-370-3

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Query Match      84.0%; Score 194; DB 14; Length 319;
Best Local Similarity 79.2%; Pred. No. 5,6e-19;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Db 23 RKAMKGLGTDSESIITLTSSNAQROEISAFAKTLFGRLDDDKSE 70

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RESULT 8
US-10-080-370-6
Sequence 6, Application US/10080370
Publication No. US2003016532A1
GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
FILE REFERENCE: SURR.90
CURRENT APPLICATION NUMBER: US/10/080,370
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,582
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 669
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
NAME/KEY: misc feature
LOCATION: (334)..(334)
OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (351)..(351)
OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (45)..(45)
OTHER INFORMATION: modified annexin gene
OTHER INFORMATION: n = a, c, g, or t
NAME/KEY: misc feature
LOCATION: (1000)..(1002)
OTHER INFORMATION: n = a, c, g, or t
NAME/KEY: misc feature
LOCATION: (1051)..(1053)
OTHER INFORMATION: n = a, c, g, or t
US-10-080-370-6

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Query Match      84.0%; Score 194; DB 14; Length 669;
Best Local Similarity 79.2%; Pred. No. 1,4e-18;
Matches 38; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Db 37 RKAMKGLGTDSESIITLTSSNAQROEISAFAKTLFGRLDDDKSE 84

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RESULT 9
US-10-097-340-10
Sequence 10, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOBBSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMADT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identifi
FILE REFERENCE: Mri-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-10

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Query Match      72.3%; Score 167; DB 14; Length 321;
Best Local Similarity 66.7%; Pred. No. 3,8e-15;
Matches 32; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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Db 26 RKAMKGLGTDSESIITLTSSNAQROEISAFAKTLFGRLDDDKSE 73

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RESULT 10
US-09-925-301-1062
Sequence 1062, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10

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NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
SEQ ID NO: 18
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-031B-18

Query Match 64.9%; Score 150; DB 15; Length 327;
Best Local Similarity 59.6%; Pred. No. 1e-12;
Matches 28; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Oy 2 KAMKLGTDSEISILTLTSSNAQROEISAAPKTLFGRLDDDKSE 48
Db 32 KAMKLGITNEQALIDVLTKRSTORQIAKSFKAQFGDLTETLKSE 78

RESULT 14

US-09-925-297-479
Sequence 479, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 479
LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (66)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-479

Query Match 57.6%; Score 133; DB 9; Length 158;
Best Local Similarity 47.9%; Pred. No. 1e-10;
Matches 23; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Oy 1 RKAMKLGTDSEISILTLTSSNAQROEISAAPKTLFGRLDDDKSE 48
Db 39 QKAIKIGTDKMLISILTLSSNAQROXIVKEYQAAVKELKDKDKD 86

RESULT 15

US-10-205-823-34
Sequence 34, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Ganavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamakar, Shubhangi
APPLICANT: Woneey, Angela M.
APPLICANT: Glat, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-34

Query Match 56.7%; Score 131; DB 14; Length 323;
Best Local Similarity 47.9%; Pred. No. 4.9e-10;
Matches 23; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Oy 1 RKAMKLGTDSEISILTLTSSNAQROEISAAPKTLFGRLDDDKSE 48
Db 28 QKAIKIGTDKMLISILTLSSNAQROXIVKEYQAAVKELKDKDKD 75

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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March 25, 2004, 08:05:00 ; Search time 46 Seconds
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US-09-787-923-2
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ssing: Minimum Match 0%

Maximum Match 100%

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No. is the number of results predicted by chance to have a
greater than or equal to the score of the result being printed,
as derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	DB	ID	Description
1600	100.0	320	13	US-10-007-761-72	Sequence 72, Appl
600	100.0	320	16	US-10-424-232-1	Sequence 1, Appli
590	99.4	327	9	US-09-970-969-2	Sequence 2, Appli
590	99.4	327	9	US-09-970-969-4	Sequence 4, Appli
590	99.4	327	9	US-09-970-969-6	Sequence 6, Appli
1.5	90.7	319	14	US-10-080-370-3	Sequence 3, Appli
1.5	90.7	669	14	US-10-080-370-6	Sequence 6, Appli
012	63.2	208	9	US-09-925-302-731	Sequence 731, App
933	58.3	321	14	US-10-097-340-10	Sequence 10, Appl
933	58.3	324	9	US-09-925-301-1062	Sequence 1062, Ap
927	57.9	675	12	US-10-114-270-160	Sequence 160, App
2.5	52.0	327	15	US-10-236-031B-18	Sequence 34, Appl
811	50.7	323	14	US-10-205-823-34	Sequence 34, Appl
781	48.8	324	14	US-10-316-253-262	Sequence 262, App
780	48.8	485	9	US-09-925-300-1664	Sequence 1664, Ap

339	44.3	708.5	9	US-09-974-298-91	Sequence 91, Appl
339	44.3	708.5	14	US-10-097-340-6	Sequence 6, Appli
339	44.3	708.5	14	US-10-097-340-8	Sequence 8, Appli
327	42.7	683	9	US-09-764-853-615	Sequence 615, App
322	42.5	680	10	US-09-764-881-110	Sequence 110, App
332	42.5	680	15	US-10-242-747-110	Sequence 110, App
319	41.2	658.5	14	US-10-304-287-2	Sequence 2, Appli
373	40.8	653	9	US-09-925-301-888	Sequence 888, App
388	40.8	653	12	US-10-276-774-2250	Sequence 2250, Ap
346	40.6	649	9	US-09-919-172-39	Sequence 39, Appl
346	40.6	649	9	US-09-974-298-93	Sequence 93, Appl
346	40.1	642	14	US-10-316-253-300	Sequence 300, App
322	36.3	581.5	15	US-10-369-493-5717	Sequence 5717, Ap
317	33.8	540	15	US-10-369-493-5695	Sequence 5695, Ap
364	31.9	511	12	US-10-425-114-59570	Sequence 59570, A
369	31.9	511	12	US-10-425-114-66547	Sequence 66547, A
330	31.9	510	12	US-10-425-114-61774	Sequence 61774, A
329	31.4	500.5	12	US-10-425-114-63278	Sequence 63278, A
326	31.3	500.5	12	US-10-424-599-257117	Sequence 257117, A
327	30.1	481.5	12	US-10-425-114-52360	Sequence 52360, A
322	29.3	469.5	12	US-10-424-599-196945	Sequence 196945, A
313	26.9	431	12	US-10-424-599-279849	Sequence 279849, A
320	26.9	431	12	US-10-425-114-55270	Sequence 55270, A
324	26.9	431	12	US-10-425-114-43962	Sequence 43962, A
314	26.9	430.5	12	US-10-424-599-279847	Sequence 279847, A
304	25.7	410.5	12	US-10-424-599-231427	Sequence 231427, A
312	25.5	408.5	12	US-10-424-599-172904	Sequence 172904, A
320	25.3	405.5	12	US-10-424-599-201908	Sequence 201908, A
316	25.1	401.5	12	US-10-424-599-144032	Sequence 144032, A
333	25.1	401.5	12	US-10-425-114-47663	Sequence 47663, A
333	25.1	401.5	12	US-10-425-114-55802	Sequence 55802, A
289	25.0	399.5	9	US-09-925-301-897	Sequence 897, App
314	24.9	398.5	12	US-10-424-599-273745	Sequence 273745, A
319	24.6	393.5	12	US-10-424-599-213299	Sequence 213299, A
173	24.2	388	12	US-10-424-599-203868	Sequence 203868, A
51	24.2	387	50	US-10-369-493-3240	Sequence 3240, Ap
52	24.0	384.5	54	US-10-425-114-60631	Sequence 60631, A
53	24.0	384.5	54	US-10-425-114-64727	Sequence 64727, A
54	24.0	384	15	US-10-104-047-2800	Sequence 2800, Ap
341	23.9	382.5	12	US-10-425-114-60513	Sequence 60513, A
344	23.9	382.5	12	US-10-425-114-59289	Sequence 59289, A
319	23.9	382	12	US-10-424-599-230318	Sequence 230318, A
449	23.9	382	15	US-10-369-493-12408	Sequence 12408, A
316	23.8	381.5	14	US-10-219-220-260	Sequence 260, App
316	23.7	378.5	14	US-10-219-220-62	Sequence 62, Appl
316	23.7	378.5	15	US-10-393-840-56	Sequence 56, Appl
316	23.7	378.5	15	US-10-393-840-114	Sequence 114, App
331	23.1	370	15	US-10-369-493-6310	Sequence 6310, Ap
333	21.7	347.5	12	US-10-425-114-40052	Sequence 40052, A
333	21.7	347.5	12	US-09-925-297-479	Sequence 479, App
158	21.0	336.5	9	US-10-369-493-13195	Sequence 13195, A
322	20.9	332	15	US-10-393-840-53	Sequence 53, Appl
213	20.8	332	15	US-10-393-840-53	Sequence 43123, A
245	17.8	284.5	12	US-10-425-114-43123	Sequence 211315, A
270	17.8	284.5	12	US-10-424-599-211315	Sequence 72654, A
333	17.1	274	12	US-10-425-114-72654	Sequence 68027, A
212	17.1	273.5	12	US-10-425-114-68027	Sequence 12654, A
241	16.6	265.5	12	US-10-393-840-55	Sequence 55, Appl
241	16.1	257.5	12	US-10-425-114-41196	Sequence 41196, A
239	15.3	245.5	14	US-10-219-220-65	Sequence 65, Appl
239	15.3	245.5	15	US-10-393-840-54	Sequence 54, Appl
239	15.3	245.5	15	US-10-393-840-54	Sequence 117, App
184	14.5	232	14	US-10-219-220-66	Sequence 66, Appl
184	14.5	232	15	US-10-393-840-118	Sequence 118, App
112	14.3	229	15	US-10-264-049-3741	Sequence 3741, Ap
184	13.9	222	15	US-10-393-840-52	Sequence 52, Appl
319	13.8	221	14	US-10-259-165-56	Sequence 56, Appl
319	13.8	221	14	US-10-259-165-56	Sequence 402, App
81	13.7	219	12	US-10-424-599-271482	Sequence 271482, A
83	13.4	219	13	US-10-259-165-290	Sequence 290, App
336	11.5	214.5	14	US-10-424-599-186704	Sequence 186704, A
186	11.5	184.5	15	US-10-264-049-2936	Sequence 2936, Ap
142	10.1	161.5	12	US-10-424-599-201914	Sequence 201914, A
100	9.4	150	12	US-10-424-599-223868	Sequence 223868, A

Sequence 951, App
Sequence 71353, A
Sequence 198302,
Sequence 279848,
Sequence 1467, Ap
Sequence 243530,
Sequence 30160, A
Sequence 952, App
Sequence 160681,
Sequence 63, Appl
Sequence 115, App
Sequence 3937, Ap

ALIGNMENTS

RESULT 1
US-10-007-761-72
; Sequence 72, Application US/10007761
; Publication No. US20020150984A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Peptides for Activation and Inhibition
; FILE REFERENCE: of delta-PK
; FILE REFERENCE: 58600-8208.US00
; CURRENT APPLICATION NUMBER: US/10/007,761
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/262,060
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-761-72

Query Match 100.0%; Score 1600; DB 13; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 60
DB 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 60
QY 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
DB 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
DB 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 181 QAGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLAV 240
DB 181 QAGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
DB 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
QY 301 KGDTSQDYKALLLCGEDD 320
DB 301 KGDTSQDYKALLLCGEDD 320

RESULT 2
US-10-424-232-1
; Sequence 1, Application US/10424232
; Publication No. US20040022731A1
; GENERAL INFORMATION:
; APPLICANT: Bogdanov, Alexei

APPLICANT: Schellenberger, Eyk
APPLICANT: Petrovsky, Alexander
APPLICANT: Josephson, Lee
TITLE OF INVENTION: In vivo Imaging of Apoptosis
FILE REFERENCE: 00786-549001
CURRENT APPLICATION NUMBER: US/10/424,232
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/60/376,052
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-424-232-1

Query Match 100.0%; Score 1600; DB 16; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 60
DB 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 60
QY 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
DB 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
DB 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
QY 181 QAGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLAV 240
DB 181 QAGELKWTDEKFTITFGTRSVSHLRKVFQKMTISGFIETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
DB 241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMI 300
QY 301 KGDTSQDYKALLLCGEDD 320
DB 301 KGDTSQDYKALLLCGEDD 320

RESULT 3
US-09-970-969-2
; Sequence 2, Application US/09970969
; Patent No. US20020103341A1
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan F.
; APPLICANT: Erown, David S.
; TITLE OF INVENTION: Amexin Derivatives with Endogenous Chelation Sites
; FILE REFERENCE: uofw-1-13841
; CURRENT APPLICATION NUMBER: US/09/970,969
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-969-2

Query Match 99.4%; Score 1590; DB 9; Length 327;
Best Local Similarity 99.7%; Pred. No. 2.2e-138;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 60
DB 8 MAQVLRGTVTDPFGFDERADAETLRKAMKGLGTDEESILTLTSSNAQRQEISAAPKTL 67

Qy	65	LLDDUKSELITGTFEKLIV	ALMAMPGRSLYDAYEL	XHALKGAGTNEKVLTEII	ASRTPEELRA	124
		::::	::::	::::	::::	
Db	63	LVNDKMSELITGTFEKLIV	ALMAMPGRSLYDAYEL	XHALKGAGTDEKVLTEII	ASRTPEELRA	122
		::::	::::	::::	::::	
Qy	125	IKQVYEEEGSSLEDDVV	GDTSYGYYQRMVLVLL	QANRPDAGIDEAQVEDQAAL	FOAGE	184
		::::	::::	::::	::::	
Db	123	IKQAYEEEGSNLEDDVV	GDTSYGYYQRMVLVLL	QANRPDPAIDDAQVELDAQAL	FOAGE	182
		::::	::::	::::	::::	
Qy	185	LKWGTDEKFIITFTRSV	SHLRKVFQKYMITSQFI	EETIDRETSGNLEQLLAV	VKSI	244
		::::	::::	::::	::::	
Db	183	LKWGTDEKFIITILTRSV	SHLRKVFQKYMITSQFI	EETIDRETSGNLENILLA	VKSI	242
		::::	::::	::::	::::	
Qy	245	RSI PAYLAETLYAMKGA	GTDHTLIRVMVSRSEID	LFNIRKFRKNFATSLYS	MIKGD	304
		::::	::::	::::	::::	
Db	243	RSI PAYLAETLYAMKGA	GTDHTLIRVIVSRSEID	LFNIRKFRKNFATSLYS	MIKGD	302
		::::	::::	::::	::::	
Qy	305	SGDYKKAALLLC -	GEDD	320		
		::::	::::	::::	::::	
Db	303	SGDYKKAALLLC	CGGEDD	319		
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RESULT 7
US-10-080-370-6
; Sequence 6, Application US/10080370
; Publication No. US20030166532A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis
; FILE REFERENCE: SURR.90
; CURRENT APPLICATION NUMBER: US/10/080,370
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
; NAME/KEY: misc_feature
; LOCATION: (334)..(334)
; OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, I
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, I
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; OTHER INFORMATION: modified annexin gene
; NAME/KEY: misc_feature
; LOCATION: (45)..(45)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (1000)..(1002)
; OTHER INFORMATION: n = a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (1051)..(1053)
; OTHER INFORMATION: n = a, c, g, or t
US-10-080-370-6

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Db	17	LRGVTFDPSGFDGADAEVLRKAMKGLGTDEDSLINLLTARSNAQROQIAEBEFTKFGD	76
Qy	65	LLDOLKSELTKFEKLIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEELRA	124
Db	77	LVDNMKSELTKFEKLIVALKMPSRLYDAVELKHALKGAGTDEKVLTEIIASRTPEELRA	136
Qy	125	IKQVYEEYGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPDAGIDEAQVEQDAQALFOAGE	184
Db	137	IKQAYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPDTAIDDAQVELDAQALFOAGE	196
Qy	185	LKWZTDBEKITITFGTRSVSHLRKVFDKYMTISGFQIETEITDRETSGNLEQALLAVKSI	244
Db	197	LKWZTDBEKITITLGTBSVSHLRVFDKYMTISGFQIETEITDRETSGNLELLAVKSI	256
Qy	245	RSIPAYLAEATLYAMKAGGTDHDLIRVMVSRSDIDLFNIRKEFRKFNATSLYSMIKGD	304
Db	257	RSIPAYLAEATLYAMKAGGTDHDLIRVSVSRSDIDLFNIRKEFRKFNATSLYSMIKGD	316
Qy	305	SGDYKKALLLC-GEDD	320
Db	317	SGDYKKALLLCGGEDD	333

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RESULT 8
US-09-925-302-731
; Sequence 731, Application US/09925302
; Patent No. US20320044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925.302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 731
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-731

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RESULT 9
US-10-097-340-10 ; Sequence 10, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: JOHJ MONAHAN

APPLICANT: Gangolli, Esha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Casman, Stacie J.
APPLICANT: Ji, Weizhen
APPLICANT: Anderson, David W.
APPLICANT: Lietze, Mario W.
APPLICANT: Rastelli, Luca
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US2004030110A1el Proteins and Nucleic Acids. Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 160
LENGTH: 675
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-270-160

Query Match 57.9%; Score 927; DB 12; Length 675;
Best Local Similarity 57.8%; Pred. No. 1.1e-76;
Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;
QY 6 RGTVTDFGDFDERADAETLRKAMKGLGTDDEESILTLTSSNAQROEISAAPKTLFGRDL 65
DB 11 RGSIHDFGDFPNQDAEALYAMKGFSGDKAEILDIITSSNRQROEVCOSKSLYKDL 70
QY 66 LDKSELTKGFKELIVALKMPSRLYDAYELHALKGAGTNEKVLTEIISRTPEELRAI 125
DB 71 IADLVKLTGKPERLIVLMRPPAYCDAKEIKDAISGIGTDEKCLIEILASRTNEQMHQL 130
QY 126 KQVVEEYSSLEDDVVGTSYQYQMLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
DB 131 VAAKDAVERDEADIDIGTSGHGFQKMLVLLQGTREDDVVSSEDLVQODVQDLYEAGEL 190
QY 186 KWTDEEKFITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIR 245
DB 191 KWTDEAQPIYTLGNRSKOHLELDFEYDKTGPKEIPASIRGELSGDFKMLAVVVKIR 250
QY 246 SIPAYLAETLYAMKAGAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMIKGTDS 305
DB 251 STPEFAERLFXAMKGLGTRDNLIRNIVSRSEIDLINLKCHFKKMYGKTLSSMIMEDTSG 310
QY 306 GDYKALLLCCGEDD 320
DB 311 GEYKTKLLKSGDD 325

RESULT 12

US-10-236-031B-18
Sequence 18, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Jensen, Roderick V.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic Tests
FILE REFERENCE: B0801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patent in version 3.1
SEQ ID NO 18
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-10-236-031B-18

Query Match 52.0%; Score 832.5; DB 15; Length 327;
Best Local Similarity 56.5%; Pred. No. 2.1e-68;
Matches 177; Conservative 48; Mismatches 87; Indels 1; Gaps 1;
QY 8 TVIDPFGDFDERADAETLRKAMKGLGTDDEESILTLTSSNAQROEISAAPKTLFGRDL 67
DB 14 TVKSSSHFNPDPDAETLYAMKGLGTDDEESILTLTSSNAQROEISAAPKTLFGRDL 73
QY 68 LDKSELTKGFKELIVALKMPSRLYDAYELHALKGAGTNEKVLTEIISRTPEELRAI 127
DB 74 TLKSELGKPERLIVLMRPPAYCDAKEIKDAISGIGTDEKCLIEILASRTNEQMHQL 133
QY 128 VVEEYSSLEDDVVGTSYQYQMLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 186
DB 134 AYEDYSSLEDDVVGTSYQYQMLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 193
QY 187 WGTDEEKFITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIR 246
DB 194 RGTDEMKFITLCTRSTHLLRVFEEVEKANKSIEDSIKSETHGSLSEALMTVVVKCTQN 253
QY 247 IPAYLAETLYAMKAGAGTDDHTLIRVMVSRSEIDLFINRKEFRKNFATSLYSMIKGTDS 306
DB 254 LHSFPAERLYAMKAGAGTDDHTLIRVMVSRSEIDLINLKCHFKKMYGKTLSSMIMEDTSG 313
QY 307 DYKALLLCCGED 319
DB 314 DYKALLLCCGED 326

RESULT 13

US-10-205-823-34
Sequence 34, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: McNahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Womsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044

APPLICATION NUMBER: US/10/205,823
FILING DATE: 2002-07-25
APPLICATION NUMBER: 60/307,982
LING DATE: 2001-07-25
APPLICATION NUMBER: 60/314,356
LING DATE: 2001-08-22
APPLICATION NUMBER: 60/325,020
LING DATE: 2001-09-25
APPLICATION NUMBER: 60/341,746
LING DATE: 2001-12-12
APPLICATION NUMBER: 60/362,158
LING DATE: 2002-03-05
LF SEQ ID NOS: 455
FAST-SEQ for Windows Version 4.0
34
323

RT
M: Homo sapiens

23-34

ch 50.7%; Score 811; DB 14; Length 323;

1 Similarity 50.2%; Pred. No. 2e-66;

159; Conservative 61; Mismatches 96; Indels 0; Gaps 0;

6 RGTVPDPGDERADAEATLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTLFGDRL 65

9 RGVIRYDPSVSDAEAIKAIKIGTDEKTLNLTSSNAQRQIVKQYQAAVYKEL 68

66 LDKKSELTKGFKELI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEELRAI 125

69 KDLKGDLSGHFEHLMVALVTPPAVFDKQLKSKMGAGTNEALTEILTRTSRQWKDI 128

26 KQYEEYSGSLEDDVVGDTSGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185

29 SQAYTYVYKSLGDISSETSGDFRKAALLTLADGRDESUKVDEHLAKQDAQILYKAGEN 188

86 KWTDEKFTITPTGTRSVHLRKVFDKYMITSQFIEETIDRTSGNLEQLLLAVVKSIR 245

89 RWGTDKFTTEILCLRSFPQKLTFDEYRNISQKDI VDSIKGELSGHFEDLLILAVNCVR 248

46 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKEFRKNFATSLYMIKGDTS 305

49 NTPAFLAHLRAKLGIGTDEFTLNRMVSRSEIDLINIRKEFRKNFATSLYSAIKSDTS 308

06 GDYKKALLLCGGDD 320

09 GDYEITLLKICGGDD 323

53-262

262, Application US/10316253

on No. US20030162706A1

INFORMATION:

T: The Procter & Gamble Company

T: Peters, Kevin

T: Thompson, Larry

T: Wang, Feng

T: Greis, Kenneth

INVENTION: Angiogenesis Modulating Proteins

ERENCE: 8865M

APPLICATION NUMBER: US/10/316,253

FILING DATE: 2002-12-10

PLICATION NUMBER: US 60/355,295

LING DATE: 2002-02-08

F SEQ ID NOS: 308

: Patent in version 3.1

262

324

RT

M: Rattus norvegicus

53-262

Query Match 48.8%; Score 781; DB 14; Length 324;

Best Local Similarity 48.3%; Pred. No. 1.2e-63;

Matches 152; Conservative 64; Mismatches 99; Indels 0; Gaps 0;

QY 6 RGTVPDPGDERADAEATLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTLFGDRL 65

Db 10 RGTINNYPGFNSVDAAIRKAIKIGTDEKTLNLTSSNAQRQIVKHIQEAQEAL 69

QY 66 LDKKSELTKGFKELI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEELRAI 125

Db 70 KADLKGDLSGHFEHVMVALITAPAVFDKQLKSKMRGMGTDEDTLIELTRTSRQWKDI 129

QY 126 KQYEEYSGSLEDDVVGDTSGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185

Db 130 SQAYTYAYKKLRDDDISSETSGDFRKAALLTLADGRDESUKVDEHLAKQDAQILYDAGEK 189

QY 186 KWTDEKFTITPTGTRSVHLRKVFDKYMITSQFIEETIDRTSGNLEQLLLAVVKSIR 245

Db 190 KWTDEKFTTEILCLRSFPQKLTFDEYRNISQKDI VDSIKGELSGHFEDLLILAVVCTR 249

QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKEFRKNFATSLYMIKGDTS 305

Db 250 NTPAFLAHLRAKLGIGTDEFTLNRMVSRSEIDLINIRKEFRKNFATSLYSAIQSDTS 309

QY 306 GDYKKALLLCGGDD 320

Db 310 GDYRTVLLKICGGDD 324

RESULT 15

US-09-925-300-1664

; Sequence 1664, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 1664

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-925-300-1664

Query Match 48.8%; Score 780; DB 9; Length 485;

Best Local Similarity 48.1%; Pred. No. 2.6e-63;

Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPFGFDERADAEATLRKAMKGLGTDEESILTLTSSNAQRQISAAFKTL 60

Db 168 VTQVTQGTIRPAANFDAIRDAEILRKAMKGFQDEQAI VDVVVRNSNDQKIKAAFKTS 227

QY 61 FGRDLLDLKSEITGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120

Db 228 YGKDILKDLKSELSGNMEELIALFMPPTYDWSLRKAMQAGTQERVLEILCTRITNQ 287

QY 121 ELRAIKQVVEEYSGSLEDDVVGDTSGYQYRMVLLQANRDPDAGIDEAQVEQDAQALF 180

Db 288 EIREIVRCYQSEFGRDLEKDIERSDTSGHFERLLVSMCOGNRDNQINHQMAQEDARLY 347

QY 181 QAQELKMGTDDEKFTITPTGTRSVHLRKVFDKYMITSQFIEETIDRTSGNLEQLLLAV 240

Db 348 QAQEGRLGTDDESCFNMLATRSFPQURATMEAYSRVANDLLSSVSREFSGVYVESGLKTI 407

QY 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLINIRKEFRKNFATSLYSMI 300

Db 408 LQCALNRDAFAERLYAMKAGTDDSTLVIRVTRSEIDLVOIKOMFAQMYQKTLGTMI 467
Qy 301 KGDTSYDYKXALLLCGE 318
Db 468 AGDTSYDYRLLLAIVGQ 485

RESULT 16
US-09-974-298-91
; Sequence 91, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hui-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 91
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 1378745CDI
US-09-974-298-91

Query Match 44.3%; Score 708.5; DB 9; Length 339;
Best Local Similarity 46.3%; Pred. No. 6.2e-57;
Matches 146; Conservative 63; Mismatches 105; Indels 1; Gaps 1;
Qy 7 GTVDFPGFDERADATLRKAMKGLGTDEESILTLLTSRNSAQRQEIISAAFKTLFGRDIL 66
Db 25 GSVKAYTNFDAERDALNIETAIKTKGVDEVITVNLITNSNAQRQDIAFAYQRRTKKELA 84
Qy 67 DDLKSELTKFKELI VALMKPSRLYDAYELKHALKAGTNEKVLTEIITASRTPEELRAIK 126
Db 85 SALKSALSGLHETVLGLLTKPAQYDASELKSMKGLGTDEDSLTEIICSRTNQELQIN 144
Qy 127 QVYEEYSGSLEDVVGGTSGYQYQRMVLVLLQANRDPDAG-IDEAQVEQDAALFOAGEL 185
Db 145 RVYKEMKYTDLEKDIISDTSGDFRKLWALAKGRAEDGSVIDYELIDQARDLDYAGVK 204
Qy 186 KWTDEEKFITFGTRSYSHLRKVFDMYKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 245
Db 205 RKGTDVPKWIISWTERSVPHLQKVFDRYKSYSPYDMLESIRKEVKGDLNENAFNLVQCIQ 264
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIKGDTS 305
Db 265 NKPLFADRLYDSMKGKGTDRKVLIRIMVSRSEVDMKIRSEFKRYKGSLSYYIQDQTK 324
Qy 306 GDYKALLLCGEDD 320
Db 325 GDYKALLLCGGDD 339

RESULT 17
US-10-097-340-6
; Sequence 6, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISY
; APPLICANT: Peter OLANDT

; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MEI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-6

Query Match 44.3%; Score 708.5; DB 14; Length 339;
Best Local Similarity 46.3%; Pred. No. 6.2e-57;
Matches 146; Conservative 63; Mismatches 105; Indels 1; Gaps 1;
Qy 7 GTVDFPGFDERADATLRKAMKGLGTDEESILTLLTSRNSAQRQEIISAAFKTLFGRDIL 66
Db 25 GSVKAYTNFDAERDALNIETAIKTKGVDEVITVNLITNSNAQRQDIAFAYQRRTKKELA 84
Qy 67 DDLKSELTKFKELI VALMKPSRLYDAYELKHALKAGTNEKVLTEIITASRTPEELRAIK 126
Db 85 SALKSALSGLHETVLGLLTKPAQYDASELKSMKGLGTDEDSLTEIICSRTNQELQIN 144
Qy 127 QVYEEYSGSLEDVVGGTSGYQYQRMVLVLLQANRDPDAG-IDEAQVEQDAALFOAGEL 185
Db 145 RVYKEMKYTDLEKDIISDTSGDFRKLWALAKGRAEDGSVIDYELIDQARDLDYAGVK 204
Qy 186 KWTDEEKFITFGTRSYSHLRKVFDMYKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 245
Db 205 RKGTDVPKWIISWTERSVPHLQKVFDRYKSYSPYDMLESIRKEVKGDLNENAFNLVQCIQ 264
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIKGDTS 305
Db 265 NKPLFADRLYDSMKGKGTDRKVLIRIMVSRSEVDMKIRSEFKRYKGSLSYYIQDQTK 324
Qy 306 GDYKALLLCGEDD 320
Db 325 GDYKALLLCGGDD 339

RESULT 18
US-10-097-340-8
; Sequence 8, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR

```
NT: Steve G. KOVATS
NT: Rachel E. MEYERS
NT: Michael MORRISSEY
NT: Peter OLANDT
NT: Ami SEN
NT: Peter VEIBY
NT: Gordon B. MILLS
NT: Robert C. BAST, Jr.
NT: Karen LU
NT: Rosemarie SCHWANDT
NT: Xumei ZHAO
NT: Karen GLATT
NT: Karen GLATT
F INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
F INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
PERENCE: MRI-030
APPLICATION NUMBER: US/10/097,340
FILING DATE: 2002-03-14
APPLICATION NUMBER: 60/276,025
FILING DATE: 2001-03-14
APPLICATION NUMBER: 60/325,149
FILING DATE: 2001-09-26
APPLICATION NUMBER: 60/276,026
FILING DATE: 2001-03-14
APPLICATION NUMBER: 60/324,967
FILING DATE: 2001/09/26
APPLICATION NUMBER: 60/311,732
FILING DATE: 2001-08-10
APPLICATION NUMBER: 60/325,102
FILING DATE: 2001-09-26
APPLICATION NUMBER: 60/323,580
FILING DATE: 2001-09-19
LNG SEQ ID NOS: 363
FAST-SEQ for Windows Version 4.0
339
PRT
M: Homo sapiens
40-8
ch 44.3%; Score 708.5; DB 14; Length 339;
1 Similarity 46.3%; Pred. No. 6.2e-57;
146; Conservative 63; Mismatches 105; Indels 1; Gaps 1;
7 GTVTDFPGFERADAETLRKAMKGLGTDSEILTLTSRNAQOEISAAFKTLFGRDLL 66
25 GSVKAYTNFDEARDALNIETAKTGVDVITVNLTRNSNAQODIAFAYQRTTKELA 84
67 DLKSELTGFEKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
85 SALKSALSGHLETVILGLLKTPAQYDASELSKAMKGLGTDSESLIETICSRTNQELQEI 144
27 QVYEEYVGSLEDDVVGDTSGYQRMVLVLLQANRDPDAG-IDEAQVEQDAQALFQAGEL 195
45 RVTKEMTKDLEKDIISDTSGDFRKLKMLAKGRRAEDGSDVIDYELDQDARDLYDAGVK 204
86 KWTGDEKFTITFGTRSVSHLRKVFQKMTISGFQIETIDRETSGNLEQLLLAVVKSIR 245
05 RKGTDPVKWISINTERSVPHLQKVFDRYKSYSPYDMLESIRKEVKGLENAFLNLVQCIC 264
46 SIPAYLAETLYAMKAGAGTDHDLIRVWVSRSEIDLNFIRKEFRKNFATSLYSMIKGDT 305
65 NKPLYFADRLYDSMKGKGTDRKVLIRVWVSRSEVDMKIRSEPKRYKGLYIYIQDDTK 324
06 GDYKALLLCGGDD 320
25 GDYQKALLVLCGGDD 339
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```
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 615
LENGTH: 327
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-853-615
Query Match 42.7%; Score 683; DB 9; Length 327;
Best Local Similarity 45.0%; Pred. No. 1.3e-54;
Matches 136; Conservative 66; Mismatches 100; Indels 0; Gaps 0;
QY 14 GFDERADAETLRKAMKGLGTDSEILTLTSRNAQOEISAAFKTLFGRDLLDLKSEL 73
DB 24 GFDVDRDAKLNKACKGMGTNEAIIELSGRTSDEROQIKQKYKATYGKELEVLKSEL 83
QY 74 TGFEKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKOVYEEY 133
DB 84 SCNFEXTALLDRPSEYAAARQLQEAAMKGLGTDESVLIEVLCRTNKEIIAIKEAYQRLF 143
QY 134 GSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGELKMGTDREK 193
DB 144 DRSLESDVKGDTSGNLKILVLLQANRNEGDVDKLAQDAKLDYDAGEGRWGTDELA 203
QY 194 FITFGTRSVSHLRKVFQKMTISGFQIETIDRETSGNLEQLLLAVVKSIRSIPIYALAE 253
DB 204 FNEVLAKRSYKQRLATFQAYQILIGKDIEAIEETSGDLOKAYLTLVRCAQDCEDYFAE 263
QY 254 TLYYAMKAGAGTDHDLIRVWVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTSGDYKCALL 313
DB 264 RLYKSMKAGAGTDEETLIRIIVTRAEVDLQGIKAKFQEKYOKSLSDMWVSRSDTSGDFRKL 323
QY 314 LL 315
DB 324 AL 325
RESULT 20
US-09-764-881-110
Sequence 110, Application US/09764881
Publication No. US20030125246A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ07
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 110
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (304)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-110
Query Match 42.5%; Score 680; DB 10; Length 332;
Best Local Similarity 45.0%; Pred. No. 2.6e-54;
Matches 136; Conservative 65; Mismatches 101; Indels 0; Gaps 0;
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Db	29	GFVDVDRDAKLNKACKGMGTNEAAIIEILSGRTSDERQIQKQYKATYKGELEEVLSSEL	88
Qy	74	TGKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAIKQVYEEY	133
Db	89	SGNFEKTALALLDRPSEYAAARQLQKAMKGLGTDDESVLIEVLTCTRNKEIITAIKEAYQRLF	148
Qy	134	GSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGELKWTGDEEK	193
Db	149	DRSLESVDKGTSGNLKKILVSLLOANRNEGDDVDKLAGQDAKDLVDAGGRWGTDELA	208
Qy	194	FITIFGTRSVSHLRKVFQKMTISGFOIEETIDRETSGNLEQLLAVVKSIRSIPAYLAE	253
Db	209	FNEVLAKRSYKQLRATFOAYQILIGKIDIEEAIEETSGDLQKAYLTLVRCQDCEDYFAE	268
Qy	254	TLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGTSGDYKCALL	313
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Qy	314	LL 315	
Db	329	AL 330	
RESULT 22			
US-10-304-287-2			
; Sequence 2, Application US/10304287			
; Publication No. US20030083234A1			
; GENERAL INFORMATION:			
; APPLICANT: Waisman, David M.			
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor			
; FILE REFERENCE: MEQ2-001			
; CURRENT APPLICATION NUMBER: US/10/304,287			
; CURRENT FILING DATE: 2002-11-26			
; PRIOR APPLICATION NUMBER: US 60/333,866			
; PRIOR FILING DATE: 2001-11-28			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: Microsoft Word			
; SEQ ID NO 2			
; LENGTH: 319			
; TYPE: PRT			
; ORGANISM: mammalian			
US-10-304-287-2			
Query Match 41.2%; Score 658.5; DB 14; Length 319;			
Best Local Similarity 44.6%; Pred. No. 2.3e-52;			
Matches 140; Conservative 57; Mismatches 98; Indels 19; Gaps 1;			
Qy	7	GTVDFPGFDERADAETLRKAMKGLGTDDEESILTLTTSRNSAQRQEIISAAFKTLFGRDLL	66
Db	25	GSVKAYTNFDAERDALNIETAIKTGVDEVITVNLITNRSNAQRQDIAPAYQRTTKELA	84
Qy	67	DDJKSLELTGKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAIK	126
Db	85	SALKGALSGLHLETVILGLLKTTPAQYDASSELKASMKGLGTDDESLIEICSRTNQELQELN	144
Qy	127	QVTEEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGELK	186
Db	145	RVTKEMYKTDLEKDIIEGDS-----VIDYELIDQDARLDYAGVXR	185
Qy	187	WGTDEKFTITPGTRSVSHLRKVFQKMTISGFOIEETIDRETSGNLEQLLAVVKSIRS	246
Db	186	KGTDPVKWISINTERSVPHLQKVFDRYKSYSPYDMLIESIRKEVKGDLNLAFLNLVQCIQN	245
Qy	247	IPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGTSG	306
Db	246	KPXYFADRLYDSMKGKGTDRKVLIRIMVSRSEVDMLKIRSEPKRYKSLYYIQDQTKG	305

Qy	14	GFDERADAETLRKAMKGLGTDDEESILTLTTSRNSAQRQEIISAAFKTLFGRDLLDDLKSEL	73
Db	29	GFVDVDRDAKLNKACKGMGTNEAAIIEILSGRTSDERQIQKQYKATYKGELEEVLSSEL	88
Qy	74	TGKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAIKQVYEEY	133
Db	89	SGNFEKTALALLDRPSEYAAARQLQKAMKGLGTDDESVLIEVLTCTRNKEIITAIKEAYQRLF	148
Qy	134	GSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGELKWTGDEEK	193
Db	149	DRSLESVDKGTSGNLKKILVSLLOANRNEGDDVDKLAGQDAKDLVDAGGRWGTDELA	208
Qy	194	FITIFGTRSVSHLRKVFQKMTISGFOIEETIDRETSGNLEQLLAVVKSIRSIPAYLAE	253
Db	209	FNEVLAKRSYKQLRATFOAYQILIGKIDIEEAIEETSGDLQKAYLTLVRCQDCEDYFAE	268
Qy	254	TLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGTSGDYKCALL	313
Db	269	RLYKSMKAGTDEETLIRIIVTRAEDVLQGIKAKFXEKYQKSLSDMVRSDTSGDFRKLIV	328
Qy	314	LL 315	
Db	329	AL 330	
RESULT 21			
US-10-242-747-110			
; Sequence 110, Application US/10242747			
; Publication No. US20040005577A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
; FILE REFERENCE: PTZ07C1			
; CURRENT APPLICATION NUMBER: US/10/242,747			
; CURRENT FILING DATE: 2002-09-13			
; PRIOR APPLICATION NUMBER: 09/764,881			
; PRIOR FILING DATE: 2001-01-17			
; PRIOR APPLICATION NUMBER: 60/179,065			
; PRIOR FILING DATE: 2000-01-31			
; PRIOR APPLICATION NUMBER: 60/180,628			
; PRIOR FILING DATE: 2000-02-04			
; PRIOR APPLICATION NUMBER: 60/214,886			
; PRIOR FILING DATE: 2000-06-28			
; PRIOR APPLICATION NUMBER: 60/217,487			
; PRIOR FILING DATE: 2000-07-11			
; PRIOR APPLICATION NUMBER: 60/225,758			
; PRIOR FILING DATE: 2000-08-14			
; PRIOR APPLICATION NUMBER: 60/220,963			
; PRIOR FILING DATE: 2000-07-26			
; PRIOR APPLICATION NUMBER: 60/217,496			
; PRIOR FILING DATE: 2000-07-11			
; PRIOR APPLICATION NUMBER: 60/225,447			
; PRIOR FILING DATE: 2000-08-14			
; PRIOR APPLICATION NUMBER: 60/218,290			
; PRIOR FILING DATE: 2000-07-14			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 192			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 110			
; LENGTH: 332			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (2)			
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (304)			
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids			
US-10-242-747-110			
Query Match 42.5%; Score 680; DB 15; Length 332;			

Db 156 YREELKRD LAKDIITSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKG 215
Qy 189 TDEEKFITIFGTRSVSHLRKVFDKYMTISGFOIBETIDRETSGNLEQLLAWKXSIR SIP 248
Db 216 TDVNVFNTILTRSYQPQLRRVFQKYTKYKHDMNKVLDLELKGDIKCLTAIVKCATSKP 275
Qy 249 AYLAETLYVAMKGAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGTSGDY 308
Db 276 AFFAEKLHQAAMKGVGTRHKALIRIMVSRSEIDMNDIKAFYQKMYGISLCOAILDETKEGY 335
Qy 309 KKALLLLCG 317
Db 336 EKILVALCG 344

Search completed: March 25, 2004, 08:08:25
Job time : 47 secs

GenCore version 5.1.6					
Copyright (c) 1993 - 2004 Compugen Ltd.					
- protein search, using sw model					
March 25, 2004, 08:03:45 ; Search time 22 Seconds					
(without alignments)					
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US-09-787-923-2					
core: 1600					
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BLOSUM62					
Gapop 10.0 , Gapext 0.5					
389414 seqs, 51625971 residues					
Number of hits satisfying chosen parameters: 389414					
seq length: 0					
seq length: 2000000000					
Maximum Match 0%					
Maximum Match 100%					
Listing first 100 summaries					
Issued Patents AA:*					
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*					
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*					
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*					
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*					
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*					
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*					
No. is the number of results predicted by chance to have a					
score greater than or equal to the score of the result being printed,					
s derived by analysis of the total score distribution.					
SUMMARIES					
Score	Query Match	Length	DB ID	Description	
600	100.0	320	1	US-08-125-746-3	
600	100.0	320	4	US-08-948-276-1	
600	100.0	320	6	5225537-4	
595	99.7	319	1	US-08-125-746-1	
590	99.4	327	4	US-09-324-096A-2	
590	99.4	327	4	US-09-324-096A-4	
590	99.4	327	4	US-09-324-096A-6	
8.5	93.0	319	4	US-08-948-276-2	
4.5	91.5	318	4	US-08-948-276-3	
7.5	91.1	319	2	US-08-149-975A-2	
933	58.3	321	4	US-08-948-276-4	
924	57.8	319	3	US-08-526-136-14	
875	54.7	503	3	US-08-526-136-2	
875	54.7	505	3	US-08-526-136-4	
811	50.7	323	4	US-08-948-276-5	
780	48.8	466	3	US-08-526-136-13	
653	40.8	346	4	US-08-948-276-6	
649	40.6	346	4	US-09-919-172-39	
8.5	37.0	324	4	US-09-010-147B-16	
261	16.3	151	4	US-09-621-976-4980	
5.5	15.3	239	4	US-09-325-932A-65	
232	14.5	184	4	US-09-325-932A-66	
128	8.0	849	4	US-09-157-257-4	
120	7.5	111	4	US-09-325-932A-63	
109	6.8	73	4	US-09-325-932A-64	
6.5	6.7	701	3	US-08-923-511-2	
28	106.5	6.7	701	4	US-09-416-874A-2
29	105.5	6.6	539	4	US-09-157-257-6
30	104.5	6.5	533	3	US-09-603-185-2
31	103.5	6.5	501	4	US-09-157-257-8
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37	99.5	6.2	1051	4	US-09-911-882-14
38	99.5	6.2	1051	4	US-09-911-888-14
39	99.5	6.2	1056	4	US-09-595-684B-29
40	99	6.2	498	4	US-08-858-207A-310
41	99	6.2	1057	3	US-09-541-782-10
42	99	6.2	1057	4	US-09-723-820-10
43	99	6.2	1057	4	US-10-270-085-10
44	98	6.1	1073	4	US-09-134-000C-6356
45	98	6.1	1270	4	US-09-581-909-3
46	96.5	6.0	1716	4	US-09-543-681A-7609
47	95.5	6.0	576	4	US-09-328-352-4832
48	95.5	6.0	900	2	US-08-630-822A-62
49	95.5	6.0	900	2	US-09-005-069-62
50	95.5	6.0	900	4	US-09-171-156A-21
51	95.5	6.0	900	4	US-09-004-730A-21
52	95.5	6.0	900	4	US-08-981-799A-21
53	95	5.9	365	4	US-09-149-476-696
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55	94.5	5.9	673	4	US-09-252-991A-28817
56	94	5.9	365	4	US-09-010-147B-24
57	93.5	5.8	1053	4	US-09-724-519-2
58	93.5	5.8	1053	4	US-09-592-037-2
59	92.5	5.8	340	2	US-08-757-653-176
60	92.5	5.8	340	2	US-08-823-516-79
61	92.5	5.8	340	2	US-08-823-516-136
62	92.5	5.8	340	3	US-08-759-038-115
63	92.5	5.8	340	3	US-08-758-314-115
64	92.5	5.8	340	4	US-09-684-938-115
65	92.5	5.8	340	4	US-09-308-825A-115
66	92	5.8	484	4	US-09-540-236-3498
67	92	5.8	938	4	US-09-252-991A-23882
68	90.5	5.7	737	4	US-09-543-681A-6489
69	90.5	5.7	1161	4	US-09-543-681A-6486
70	90	5.6	359	4	US-09-134-001C-4760
71	90	5.6	382	4	US-09-800-729-206
72	90	5.6	760	4	US-09-252-991A-25928
73	90	5.6	1057	4	US-09-428-156B-2
74	89.5	5.6	663	3	US-08-776-265-5
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79	88.5	5.5	2285	4	US-09-308-375-2
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83	87.5	5.5	457	3	US-09-120-365-72
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85	87.5	5.5	1074	4	US-09-004-838-111
86	87	5.4	615	4	US-09-543-681A-8049
87	87	5.4	712	4	US-09-543-681A-8147
88	87	5.4	754	4	US-09-328-352-6501
89	87	5.4	2089	1	US-08-418-893D-23
90	87	5.4	2089	1	US-08-418-893D-24
91	87	5.4	3878	4	US-09-914-259-11
92	86.5	5.4	284	4	US-09-914-259-56
93	86.5	5.4	400	1	US-07-730-953-2
94	86.5	5.4	441	4	US-09-328-352-5426
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96	86	5.4	260	4	US-09-647-514-4
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99	86	5.4	391	4	US-09-647-514-6
100	86	5.4	391	4	US-09-647-514-13

ALIGNMENTS

RESULT 1
US-08-125-746-3

; Sequence 3, Application US/08125746
; Patent No. 5591633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IWASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 037227/1987
; FILING DATE: 20-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 184428/1987
; FILING DATE: 23-JUL-1987

; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5591633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 80-074-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELE: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLESCALE TYPE: protein

US-08-125-746-3

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Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
QY 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALF 180
DB 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQVEQDAQALF 180

QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVFDPKMYTISGFOIEETIDRETSGNLEQLLAV 240
DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVFDPKMYTISGFOIEETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
DB 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
QY 301 KGDTSGDYKKALLLCGEDD 320
DB 301 KGDTSGDYKKALLLCGEDD 320

RESULT 2

US-08-948-276-1
; Sequence 1, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 320
; TYPE: PRT
; ORGANISM: human
US-08-948-276-1

Query Match 100.0%; Score 1600; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 FGRDLLDDKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
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DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVFDPKMYTISGFOIEETIDRETSGNLEQLLAV 240
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DB 241 VKSIRSIIPAYLAETLYYAMKAGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
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DB 301 KGDTSGDYKKALLLCGEDD 320

RESULT 3

5225537-4
; Patent No. 5225537
; APPLICANT: POSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,082
; FILING DATE: 29-DEC-1989
; SEQ ID NO: 4
; LENGTH: 320
5225537-4

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320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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01 KGDTSGDYKKALLLGCEDD 320
01 KGDTSGDYKKALLLGCEDD 320
46-1
1. Application US/08125746
5591633
INFORMATION:
ANT: SAINO, YUSHI
ANT: IWASAKI, AKIO
ANT: SUDA, MAKOTO
OF INVENTION: ANTICOAGULANT POLYPEPTIDE
OF SEQUENCES: 5
PONDENCE ADDRESS:
ESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ESSEE: P.C.
ET: 1755 S. Jefferson Davis Highway, Suite 400
Arlington
E: Virginia
TRY: U.S.A.
22202
ER READABLE FORM:
UM TYPE: Floppy disk
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
WARE: Patent in Release #1.0, Version #1.25
T APPLICATION DATA:
ICATION NUMBER: US/08/125,746
NG DATE: 24-SEP-1993
SIFICATION: 530
APPLICATION DATA:
ICATION NUMBER: US 07/807,623
NG DATE: 13-DEC-1991
APPLICATION DATA:
ICATION NUMBER: JP 037227/1987
NG DATE: 20-FEB-1987
APPLICATION DATA:
ICATION NUMBER: JP 184428/1987
NG DATE: 23-JUL-1987
EX/AGENT INFORMATION:
: Oblon, No. 5591633man F.
STRATION NUMBER: 24,618
RENCE/DOCKET NUMBER: 80-074-0 DIV
MMUNICATION INFORMATION:
PHONE: (703) 413-3000
FAX: (703) 413-2220

TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-125-746-1
Query Match 99.7%; Score 1595; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.9e-143;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AQVLGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAFAKTLF 61
Db 1 AQVLGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAFAKTLF 60
QY 62 GRDLLDDLLKSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 121
Db 61 GRDLLDDLLKSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
QY 122 LRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
Db 121 LRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
QY 182 AGELKMGTDDEEKFTIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAVV 241
Db 181 AGELKMGTDDEEKFTIFGTRSVSHLRKVPDKYMTISGFOIETIDRETSGNLEQLLAVV 240
QY 242 KSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIK 301
Db 241 KSIRIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFATSLYSMIK 300
QY 302 GDTSGDYKKALLLGCEDD 320
Db 301 GDTSGDYKKALLLGCEDD 319
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US-09-324-096A-2
; Sequence 2, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 99.7%; Pred. No. 5.9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQVLGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAFAKTL 60
Db 8 MAQVLGTVTDFPGFDERADAETLRKAMKGLGTDDEESILTLTSSNAQOEISAFAKTL 67
QY 61 FGRDLLDDLLKSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
Db 68 FGRDLLDDLLKSELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
QY 121 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
Db 128 ELRAIKQVYEEYEGSSLEDDVVGDTSGYYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187

181 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 240
188 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 247
241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 300
248 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 307
301 KGDTSGDYKKALLLSCGDD 320
308 KGDTSGDYKKALLLSCGDD 327
RESULT 6
US-09-324-096A-4
; Sequence 4, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-4

Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 5,9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTL 60
8 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTL 67
61 FGRDLLDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
68 FGRDLLDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
121 ELRAIKQVYEEYGSLSDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
128 ELRAIKQVYEEYGSLSDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 187
181 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 240
188 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 247
241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 300
248 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 307
301 KGDTSGDYKKALLLSCGDD 320
308 KGDTSGDYKKALLLSCGDD 327

RESULT 7
US-09-324-096A-6
; Sequence 6, Application US/09324096A
; Patent No. 6323313
; GENERAL INFORMATION:
; APPLICANT: Tait, Jonathan
; APPLICANT: Brown, David
; TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
; FILE REFERENCE: UOFW-1-13841
; CURRENT APPLICATION NUMBER: US/09/324,096A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-096A-6
Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 5,9e-143;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTL 60
8 MAQVLRGTVTFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTL 67
61 FGRDLLDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 120
68 FGRDLLDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPE 127
121 ELRAIKQVYEEYGSLSDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALF 180
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181 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 240
188 QAGELKWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAV 247
241 VKSIRSIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMI 300
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301 KGDTSGDYKKALLLSCGDD 320
308 KGDTSGDYKKALLLSCGDD 327
RESULT 8
US-09-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
US-08-948-276-2
Query Match 93.0%; Score 1488.5; DB 4; Length 319;
Best Local Similarity 94.0%; Pred. No. 2.5e-133;
Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;
6 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTLFGRDL 65
4 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLTSRSNAQOEISAAFKTLFGRDL 63
66 LDDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRAI 125
64 VDDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELSAI 123
126 KQVYEEYGSLSDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
124 KQVYEEYGSLSDDVVGDTSGYYQRMVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 183
186 KWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAVVKSIR 245
184 KWTDEKFTTIFGTRSVSHLRKVFQKYMVTSISGFOIETIDRETSGNLEQLLAVVKSIR 243

246 SIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGDTS 305
244 SIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGDTS 303
306 GDYKALLLLC-GEED 320
304 GDYKALLLLC-GEED 319
276-3
3, Application US/08948276
INFORMATION:
ANT: Ernst, Joel D.
F INVENTION: GFP-Annexin Fusion Proteins
REFERENCE: UCSF97-113
APPLICATION NUMBER: US/08/948,276
FILING DATE: 1997-10-09
OF SEQ ID NOS: 6
E: PatentIn Ver. 2.0
3
318
SM: rat
PRT
276-3
ch 91.5%; Score 1464.5; DB 4; Length 318;
al Similarity 92.1%; Pred. No. 4.7e-131;
292; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
5 LRGTVDPPGDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGD 64
2 LRGTVDPPGDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGD 61
65 LDDLSKSLTCKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 124
62 LVNDMSKSLTCKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 121
25 IKVYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQQEODAAQALFOAGE 184
22 IKVYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQQEODAAQALFOAGE 181
85 LKGTDEEKFTITIGTRSVSHLRKVFQKMTISGFOEETIDRETSGNLELLAVVKS 244
82 LKGTDEEKFTITIGTRSVSHLRKVFQKMTISGFOEETIDRETSGNLELLAVVKS 241
45 RSIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGD 304
42 RSIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGD 301
05 GDYKALLLLC-GEED 320
02 GDYKALLLLC-GEED 318

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,975A
FILING DATE: 11-NOV-1993
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04843/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-149-975A-2
Query Match 91.1%; Score 1457.5; DB 2; Length 319;
Best Local Similarity 91.8%; Pred. No. 2.2e-130;
Matches 291; Conservative 12; Mismatches 13; Indels 1; Gaps 1;
QY 5 LRGTVDPPGDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGD 64
Db 3 LRGTVDPPGDERADAEIIRKAMKGLGTDEESILTLTSSNAQROEISAAFKTLFGD 62
QY 65 LDDLSKSLTCKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 124
Db 63 LVNDMSKSLTCKPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIISRTPEELRA 122
QY 125 IKVYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQQEODAAQALFOAGE 184
Db 123 IKVYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQQEODAAQALFOAGE 182
QY 185 LKGTDEEKFTITIGTRSVSHLRKVFQKMTISGFOEETIDRETSGNLELLAVVKS 244
Db 183 LKGTDEEKFTITIGTRSVSHLRKVFQKMTISGFOEETIDRETSGNLELLAVVKS 242
QY 245 RSIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGD 304
Db 243 RSIPAYLAETLYAMKAGTDDHTLIRVMSRSEIDLNFIRKFRKNFATSLYSIMKGD 302
QY 305 GDYKALLLLC-GEED 320
Db 303 GDYKALLLLC-GEED 319
RESULT 11
US-08-948-276-4
Sequence 4, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 321
TYPE: PRT
ORGANISM: human
US-08-948-276-4

Query Match 58.3%; Score 933; DB 4; Length 321;
Best Local Similarity 58.6%; Pred. No. 1.5e-80;
Matches 184; Conservative 53; Mismatches 77; Indels 0; Gaps 0;

Qy 7 GTVTDFFGDERADAETLRKAMKGLGTDEESILTLTTSRSNAQOEISAAPKTLFGRDLL 66
Db 8 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAVNTAQOEIRTAQKSTIGRDLI 67
Qy 67 DDLKSELTKGPEKLIIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASTPPELRAIK 126
Db 68 DDLKSELGSEFQVILGVMTPTVLYDQELRRAMKAGTDEGCLIEILASRTPEIRIS 127
Qy 127 QVYEEYSSLEDVVGTSYQYQRMVLVLOANRDPDAGIDEAQVEQDAALFOAGELK 186
Db 128 QTYQOQYGRSLEDDIRSDTSFMFORVLVLSAGGRDEGNYLDDALVRODAQDLYEAGEKK 187
Qy 187 WGTDEEKPTITFTGTRSVHLKRVDPKMYTISGFOIEETIDRETSGNLEQLLAVVKIRS 246
Db 188 WGTDEVKFLTVLCSENRNHLHVFDEYKRIEQKQIEQSIKSETSGSFEDALLAIVKCMRN 247
Qy 247 IPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKNFATSLYSMIKGDTS 306
Db 248 KSAFAYELKYSKMGKGLGDDTLIRVMVSRABIDMLDIRAHFKRLYKSLYSFIKGDTS 307
Qy 307 DYKALLLLCGEDD 320
Db 308 DYKVLVLLCGDD 321

RESULT 12
US-08-526-136-14
; Sequence 14, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319
; TYPE: amino acid

Db 189 RWGTDKFTFELCLRSFPQKLTDFEYRNISQKDIVDSIKGELSGHPEDLLLAIVNCR 248
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFNKFNATSLYMIKGDTS 305
Db 249 NTPAFLAERLHAKLGIGTDEFTLNIRVSRSEIDLDIRTEFKKHGYSLYSAIKSDTS 308
Qy 306 GDYKALLCGEDD 320
Db 309 GDYEITLLKICGDD 323

RESULT 16
US-08-526-136-13
; Sequence 13, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; US-08-526-136-13

Query Match 48.8%; Score 780; DB 3; Length 466;
Best Local Similarity 48.1%; Pred. No. 8.5e-66;
Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;
Qy 1 MAQVLRGTVDFFPGFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAFKTL 60
Db 149 VTQVQTGTIRPAANFDAIRDAEILRKAMKGFDTDEQAIVDVVANRSDQRKIKAPKTS 208
Qy 61 FGRDLLDKSELTKGFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
Db 209 YGKDLIKLSELGNNMEELILALFMPPTYDAWSLRKAMQAGTQERVLIELCTRTNQ 269
Qy 121 ELRAIKQVYEEYSGSLEDVVGDTSGVYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
Db 269 EIREIVRCYQSEFGRDLKEDIRSDTSGHFPERLLVSMCGNDRNQSIHQMAQEDAQRLY 328

Qy 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPKDKYMTISGFOIETIDRETSGNLEQLLAV 240
Db 329 QAGEGRIGTDESCFNMLATRSPPQLRATMEAYSRRMANRDLSSVSREFSGYVESGLKTI 388
Qy 241 VKSIRSPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFNKFNATSLYMI 300
Db 389 LQCALNRPAFAERLYYAMKAGTDDSTLVRIVVTRSEIDLVIQKQFAQMYQKTLGTMI 448
Qy 301 KGDTSGDYKALLLCCG 318
Db 449 AGDTSGDYRRLLAIVGQ 466

RESULT 17
US-08-948-276-6
; Sequence 6, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: UCSF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: human
; US-08-948-276-6

Query Match 40.8%; Score 653; DB 4; Length 346;
Best Local Similarity 44.3%; Pred. No. 6.4e-54;
Matches 137; Conservative 59; Mismatches 113; Indels 0; Gaps 0;
Qy 9 VTDFPFDERADAETLRKAMKGLGTDEESILTLTSRNSAQOEISAAFKTLFGRLDLD 68
Db 36 VSPYTFPFSSDVAALHKAIMVKGVDDEATIIDILTKRNNAQOQIKAAVLOETGKPLDET 95
Qy 69 LKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAIKOV 128
Db 96 LKCAULTGHLEEVVALLTPAQFADDELRAAMKGLGTDEDTLIEILASRTNKEIRDINRV 155
Qy 129 YEEYEGSSLEDVVGDTSGVYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGELKMG 188
Db 156 YREELKRDLDKIDTSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKG 215
Qy 189 TDEEKEFTITFGTRSVSHLRKVPKDKYMTISGFOIETIDRETSGNLEQLLAVVKSIRSP 248
Db 216 TDVNVNTILTRSYPPQLRRVFOKYTKYKSHDMKNVLDLELKGDIKCLTAIVKCATSKP 275
Qy 249 AYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKFNKFNATSLYMIKGTSGDY 308
Db 276 AFPAEKLHQAAMKGVGTRHKAIRIMVSRSEIDMNDIKAFYQKMYGSIQCAILDETKGDY 335
Qy 309 KKALLLLCG 317
Db 336 EKILVALCG 344

RESULT 18
US-09-919-172-39
; Sequence 39, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469

Db 76 LVVLSLDPADRDAYLANEATKRWTSNQVLMETACTRSPOLLMARQAYHARYKSMEE 135
Qy 140 DVGDTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQ-AGELKMGWDEKFTIF 198
Db 136 DVAHHTTGDFRKLVLPLGSSYRNDGDEVNMTLAKAEAKILHEKISEKAYG--HEDLIRIL 193
Qy 199 GTRSVSHURKVPDKYMTISGQIEETIDRETSGNLEQLLAVVKSIRSIPAYLAETLYA 258
Db 194 ATRSKAQVNATNLNHYKNFNGNDKDLTDPKDAFLTLIRATVKCLTRPEKYFEKVLRLA 253
Qy 259 MKGAGTDHTLIRVMVSSEIDLNFIRKFRKFNATSLYSMIKGDTSQDYKKALLLGG 317
Db 254 INKRGTDGALRVVATRAEVDMPFISEYQRRNSIPLDRAIVKDTTGDYKEMILLALIG 312

RESULT 21

US-09-621-976-4980
; Sequence 4980, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 4980

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-621-976-4980

Query Match 16.3%; Score 261; DB 4; Length 151;
Best Local Similarity 38.4%; Pred. No. 3.3e-17;
Matches 56; Conservative 29; Mismatches 61; Indels 0; Gaps 0;

Qy 174 ODAQALFOAGELKWTGDEKFTITRGSVSHLRKVPDKYMTISGQIEETIDRETSGNL 233
Db 4 QDAMVLEACQOKTEGHEKMLQMLCNKSYQQLRLVFOEFQNISQDMDVDAINECYDGYF 63
Qy 234 EQLLAVVKSIRSIPAYLAETLYAMKAGAGTDDHTLIRVMVSRSEIDLNFIRKFRKNFA 293
Db 64 QELLAIVLCVDEKPAYFAYRLYSIAHDFGPHNKTVIRILIAARSEIDLTLTKRYERYG 123
Qy 294 TSLYSMIKGDTSQDYKKALLLGGED 319
Db 124 KSLFHDIRNFASCHYKKALLAICAGD 149

RESULT 22

US-09-325-932A-65

; Sequence 65, Application US/09325932A

; Patent No. 6451604

; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry

; APPLICANT: Lasham, Annette

; TITLE OF INVENTION: Compositions affecting programmed cell

; TITLE OF INVENTION: death and their use in the modification of forestry plant develo

; FILE REFERENCE: 1022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 65

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Pinus radiata

US-09-325-932A-65

Query Match 15.3%; Score 245.5; DB 4; Length 239;

Best Local Similarity 28.9%; Pred. No. 1.9e-15;
Matches 65; Conservative 46; Mismatches 113; Indels 1; Gaps 1;

Qy 20 DAETLRKAMKGLGTDEESILTLTSRNAQOEISAAFKTLFGRDLLDDLLKSELTKGPEK 79
Db 16 DAEQLQKAFAGWGTNEILLIISILPHRNAQKVIQRYAETYGEDLLKALDKELSSDPER 75
Qy 80 LIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKOVYEEYSSLED 139
Db 76 SVLLWTLDPADRDPAFLSNEATKRLTSSNWVLMETACTRSSMELPMVROAYHARYKKSLEE 135
Qy 140 DVGDTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQAGELKMGWDEKFTIFG 199
Db 136 DIAVHTTGDPRKLLVPLASTFRYEGPEVNMTLARSEAKILHEKIHKEK-AYNHDELIRIVT 194
Qy 200 TRSVSHLRKVPDKYMTISGQIEETIDRETSGNLEQLLAVVKS 244
Db 195 TRSKAQVNATNLNHYKNFNGNDKDLTDPKDAFLTLIRATVKCLTRPEKYFEKVLRLA 239

RESULT 23

US-09-325-932A-66

; Sequence 66, Application US/09325932A

; Patent No. 6451604

; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry

; APPLICANT: Lasham, Annette

; TITLE OF INVENTION: Compositions affecting programmed cell

; TITLE OF INVENTION: death and their use in the modification of forestry plant develo

; FILE REFERENCE: 1022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 66

; LENGTH: 184

; TYPE: PRT

; ORGANISM: Pinus radiata

US-09-325-932A-66

Query Match 14.5%; Score 232; DB 4; Length 184;
Best Local Similarity 35.0%; Pred. No. 2.5e-14;
Matches 57; Conservative 33; Mismatches 73; Indels 0; Gaps 0;

Qy 20 DAETLRKAMKGLGTDEESILTLTSRNAQOEISAAFKTLFGRDLLDDLLKSELTKGPEK 79
Db 16 DSELRKAFEGWGTNEKSIILGHRTAAQKVIQRYAETYGEDLLKALDKELSSDPER 75
Qy 80 LIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKOVYEEYSSLED 139
Db 76 AVFLWTLDPADRDPAFLSNEATKRLTSSNWVLMETACTRSSMELPMVROAYHARYKKSLEE 135
Qy 140 DVGDTSGYQYQRMVLLQANRDPDAGIDEAQVQDAQALFQ 182
Db 136 DVAHTSGNFRKLLVALVSVRYEGPEVDMHLASVEAKKUSE 178

RESULT 24

US-09-157-257-4

; Sequence 4, Application US/09157257

; Patent No. 6375954

; GENERAL INFORMATION:

; APPLICANT: Dutta, Sukanta K.

; APPLICANT: Biswas, Biswajit

; APPLICANT: VENULAPALLI, Ramesh

; TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR

; TITLE OF INVENTION: POTOMAC HORSE FEVER

; FILE REFERENCE: 8172-9016

; CURRENT APPLICATION NUMBER: US/09/157,257

; CURRENT FILING DATE: 1998-09-18

; EARLIER APPLICATION NUMBER: 60/059,252

; EARLIER FILING DATE: 1997-09-18

; NUMBER OF SEQ ID NOS: 48

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GenCore version 5.1.6
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- protein search, using sw model

March 25, 2004, 08:00:30 ; Search time 45 Seconds
(without alignments)
2243.685 Million cell updates/sec

US-09-787-923-2
re: 1600
1 MAQVLGTVTDFFGDERAD.....KGDTSDYKALLLCGEDD 320

le: BLOSUM62
Gapop 10.0 ; Gapext 0.5

1017041 seqs, 315518202 residues

r of hits satisfying chosen parameters: 1017041

seq length: 0
seq length: 2000000000

sing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp Vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriaph.*

17: sp_archaeap.*

No. is the number of results predicted by chance to have a
greater than or equal to the score of the result being printed,
s derived by analysis of the total score distribution.

SUMMARIES

Score	Query Match	Length	DB	ID	Description
595	99.7	320	4	Q8WV69	Q8WV69 homo sapien
4.5	92.8	319	11	Q99LAI	Q99LAI mus musculus
390	86.9	302	11	O70371	O70371 rattus norv
255	78.4	318	13	Q78Z19	Q78Z19 xenopus lae
255	78.4	351	13	Q72V99	Q72V99 xenopus lae
052	65.8	317	13	Q93445	Q93445 oryzias lat
027	64.2	317	13	Q803A1	Q803A1 brachydania
025	64.1	317	13	Q804G6	Q804G6 brachydania
942	58.9	476	11	Q8CEX0	Q8CEX0 mus musculus
942	58.9	667	11	Q99JX6	Q99JX6 mus musculus
940	58.8	673	11	Q8BSS4	Q8BSS4 mus musculus
925	57.8	319	11	Q7TMN7	Q7TMN7 mus musculus
915	57.2	483	13	Q7T391	Q7T391 brachydania
876	54.8	320	13	Q804G4	Q804G4 brachydania
866	54.1	508	13	O93447	O93447 oryzias lat

17	862	53.9	485	13	Q804G3	Q804g3 brachydania
18	859	53.7	321	13	Q90X16	Q90x16 xenopus lae
19	857	53.6	503	11	Q921F1	Q921f1 mus musculus
20	855	53.4	321	13	Q804G7	Q804g7 brachydania
21	841.5	52.6	327	11	Q8K2N9	Q8k2n9 mus musculus
22	837.5	52.3	327	6	Q95L54	Q95l54 bos taurus
23	823.5	51.5	327	6	O97529	O97529 oryctolagus
24	809	50.6	323	11	Q8C1X9	Q8c1x9 mus musculus
25	774	48.4	463	11	Q922A2	Q922a2 mus musculus
26	771	48.2	463	11	Q8VIN2	Q8vin2 rattus norv
27	770	48.1	463	11	Q8BP75	Q8bp75 mus musculus
28	753	47.1	324	5	Q8IGJ8	Q8igj8 drosophila
29	752	47.0	324	5	Q9NL61	Q9nl61 bombyx mori
30	744.5	46.5	301	11	Q921D0	Q921d0 mus musculus
31	725	45.3	323	5	Q9NL59	Q9nl59 bombyx mori
32	719	44.9	324	5	Q9NG55	Q9ng55 drosophila
33	716	44.8	321	5	Q8WPG9	Q8wpg9 bombyx mori
34	715	44.7	486	5	Q8WPH0	Q8wph0 bombyx mori
35	711	44.4	323	5	Q9NGG6	Q9ngg6 bombyx mori
36	707	44.2	323	5	Q9NL60	Q9nl60 bombyx mori
37	706	44.1	497	5	Q27512	Q27512 caenorhabdi
38	704.5	44.0	339	4	Q8T8V2	Q8tbv2 homo sapien
39	703	43.9	338	13	Q7S298	Q7sz98 xenopus lae
40	700	43.8	324	5	Q969D3	Q969d3 drosophila
41	696.5	43.5	339	11	Q9CZ17	Q9czi7 mus musculus
42	688.5	43.0	340	13	Q7ZXM2	Q7zxm2 xenopus lae
43	685	42.8	315	5	Q95V57	Q95v57 artemia san
44	680	42.5	317	11	Q99JG3	Q99jg3 mus musculus
45	677	42.3	340	13	Q7T3A8	Q7t3a8 brachydania
46	676	42.2	340	13	Q804H2	Q804h2 brachydania
47	673	42.1	357	6	Q8WJB5	Q8wjb5 oryctolagus
48	667	41.7	337	13	Q93446	Q93446 oryzias lat
49	664.5	41.5	330	5	Q86DV3	Q86dv3 schistosoma
50	663	41.4	341	13	Q804H0	Q804h0 brachydania
51	658.5	41.2	343	13	Q7SZ11	Q7sz11 xenopus lae
52	656	41.0	322	5	Q9VXG4	Q9vxg4 drosophila
53	656	41.0	511	5	Q9VXG3	Q9vxg3 drosophila
54	653	40.8	346	6	Q8HZM6	Q8hzm6 equus cabal
55	646	40.4	316	13	Q98SH7	Q98sh7 brachydania
56	635.5	39.7	314	13	Q92128	Q92128 xenopus lae
57	630.5	39.4	337	13	Q804G9	Q804g9 brachydania
58	620	38.8	342	13	Q804H1	Q804h1 brachydania
59	617	38.6	337	13	Q804G8	Q804g8 brachydania
60	609	38.1	290	13	Q804G2	Q804g2 brachydania
61	581.5	36.3	322	5	Q27864	Q27864 caenorhabdi
62	573.5	35.8	415	11	Q8CCV9	Q8ccv9 mus musculus
63	572	35.8	209	11	Q8BSL2	Q8bsl2 mus musculus
64	558.5	34.9	337	13	Q7ZWX0	Q7zwx0 xenopus lae
65	540	33.8	317	5	Q27473	Q27473 caenorhabdi
66	530	33.1	345	4	Q9HBJ6	Q9hbj6 homo sapien
67	528.5	33.0	222	11	Q99KH3	Q99kh3 mus musculus
68	528	33.0	365	5	Q9XY89	Q9xy89 schistosoma
69	524.5	32.8	180	13	O57570	O57570 brachydania
70	520	32.5	345	11	Q9CQS1	Q9cqs1 mus musculus
71	515.5	32.2	347	5	Q9XZL9	Q9xzl9 taenia soli
72	511	31.9	316	10	Q9C9X3	Q9c9x3 arabidopsis
73	509.5	31.8	331	5	Q9BI01	Q9bi01 globodera p
74	508.5	31.8	304	11	Q9D272	Q9d272 mus musculus
75	508.5	31.8	346	5	Q9NGU7	Q9ngu7 taenia soli
76	507	31.7	316	10	Q9CSV4	Q9csv4 arabidopsis
77	504	31.5	276	4	Q96H89	Q96h89 homo sapien
78	491.5	30.7	321	10	Q84Q48	Q84q48 oryza sativ
79	489	30.6	196	11	Q9R0V2	Q9r0v2 mus musculus
80	472.5	29.5	333	10	Q9ZR53	Q9zr53 medicago sa
81	458.5	28.7	341	5	Q8ITJ0	Q8itj0 heterodera
82	451.5	28.2	316	10	Q9ZR07	Q9zru7 capsicum an
83	448	28.0	334	10	Q9FUG5	Q9fug5 ceratopter
84	435.5	27.2	316	10	Q9XEN8	Q9xen8 nicotiana t
85	427	26.7	330	10	Q9FUG6	Q9fug6 ceratopter
86	426.5	26.7	256	13	Q8AVS3	Q8avs3 xenopus lae
87	424	26.4	313	10	O65848	O65848 medicago tr
88	413	25.9	315	10	P93158	P93158 gossypium h
89	406.5	25.4	472	3	O59907	O59907 neurospora

90 405.5 25.3 321 10 Q9ZVJ7 arabidopsis
91 404 25.2 315 10 O81535 lycopersico
92 400.5 25.2 308 10 Q42922 medicago sa
93 400.5 25.0 321 10 Q9SE45 arabidopsis
94 397.5 24.8 314 10 Q24132 nicotiana t
95 391.5 24.5 318 10 Q9CSV3 arabidopsis
96 391 24.4 317 10 Q96527 arabidopsis
97 390.5 24.4 318 10 Q9LX08 arabidopsis
98 390 24.4 317 10 Q9SV70 arabidopsis
99 389.5 24.3 314 10 Q24131 nicotiana t
100 386.5 24.2 314 10 O81536 lycopersico

ALIGNMENTS

RESULT 1
Q8WV69 PRELIMINARY; PRT; 320 AA.
AC Q8WV69;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Annexin A5.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC -!- CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC018671; AAH18671.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR PRINTS; PR00191; annexin; 4.
DR ProDom; PD000143; Annexin.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 320 AA; 35924 MW; 45FAC411DDBA4D1A CRC64;

Query Match 99.7%; Score 1595; DB 4; Length 320;
Best Local Similarity 99.7%; Pred. No. 4.8e-107;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAQVLRTGVTDPGDFERADAEATLRKAMKGLGTDEESILTLTSSNAQROEISAAFTL 60
DB 1 MAQVLRTGVTDPGDFERADAEATLRKAMKGLGTDEESILTLTSSNAQROEISAAFTL 60
QY 61 FGRDLDDLKSLTCKPEKLI VALMKPSRLYDAYELKHALKAGNNEKVLTEI ASRTPE 120
DB 61 FGRDLDDLKSLTCKPEKLI VALMKPSRLYDAYELKHALKAGNNEKVLTEI ASRTPE 120
QY 121 ELRAIKQVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEA QVQDAQALF 180
DB 121 ELRAIKQVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEA QVQDAQALF 180
QY 181 QAGELKWTGDEKFTITFTGRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAV 240
DB 181 QAGELKWTGDEKFTITFTGRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAV 240
QY 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLNFIRKFRKNFATSLYSMI 300
DB 241 VKSIRSIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLNFIRKFRKNFATSLYSMI 300

QY 301 KGDTSGDYKKALLLLCGEDD 320
DB 301 KGDTSGDYKKALLLLCGEDD 320
RESULT 2
Q99LAI PRELIMINARY; PRT; 319 AA.
AC Q99LAI;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Annexin A5.
GN ANXA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC -!- CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; BC003716; AAH03716.1; -.
DR HSSP; P14668; IAB8.
DR MGD; MGI:106008; Anxa5.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 319 AA; 35738 MW; 52E2C7CCEA386917 CRC64;
Query Match 92.8%; Score 1484.5; DB 11; Length 319;
Best Local Similarity 93.7%; Pred. No. 4.5e-99;
Matches 296; Conservative 9; Mismatches 10; Indels 1; Gaps 1;
QY 6 RGTVTDPGDFERADAEATLRKAMKGLGTDEESILTLTSSNAQROEISAAFTLFGDDL 65
DB 4 RGTVTDPGDFERADAEATLRKAMKGLGTDEESILTLTSSNAQROEISAAFTLFGDDL 63
QY 66 LDDLKSLTCKPEKLI VALMKPSRLYDAYELKHALKAGNNEKVLTEI ASRTPEELRAI 125
DB 64 VDDLKSLTCKPEKLI VALMKPSRLYDAYELKHALKAGNNEKVLTEI ASRTPEELSAI 123
QY 126 KQVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEA QVQDAQALFOAGEL 185
DB 124 KQVVEEYGSLSLEDDVVGDTSGYYQRMVLVLLQANRPDAGIDEA QVQDAQALFOAGEL 183
QY 186 KWTGDEKFTITFTGRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAVKVSIR 245
DB 184 KWTGDEKFTITFTGRSVSHLRKVFYDKYMTISGFQIETIDRETSGNLEQLLAVKVSIR 243
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLNFIRKFRKNFATSLYSMIKGDTS 305
DB 244 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSIDLNFIRKFRKNFATSLYSMIKGDTS 303
QY 306 GDYKALLLLC-GEDD 320
DB 304 GDYKALLLLCGEDD 319
RESULT 3
O70371

PRELIMINARY; PRT; 302 AA.

1-1998 (TrEMBLrel; 07, Created)
 1998 (TrEMBLrel; 07, Last sequence update)
 -2003 (TrEMBLrel; 25, Last annotation update)
 protein V (Fragment).
 3 norvegicus (Rat).
 taxID=10116;
 ICE FROM N.A.
 =Lung;
 IE=9262163; PubMed=10329451;
 , Edelman J.L., Kang T., Sachs G.;
 ortin V may function as a signaling protein for vascular
 elial growth factor receptor-2/Flk-1.;
 m. Biophys. Res. Commun. 258:713-721(1999).
 MAIN: A PAIR OF ANNEKIN REPEATS MAY FORM ONE BINDING SITE FOR
 ALCTUM AND PHOSPHOLIPID (BY SIMILARITY).
 MILIARY: BELONGS TO THE ANNEKIN FAMILY.
 MILIARY: CONTAINS 4 ANNEKIN REPEATS.
 AF051895; AAC06290.1; -;
 P14668; IAB8.
 :0005509; F:calcium ion binding; IEA.
 :0005544; F:calcium-dependent phospholipid binding; IEA.
 ro; IFR001464; Annexin.
 PF00191; annexin; 4.
 ; PR00196; ANNEKIN.
 ; PD000143; Annexin; 4.
 ; SM00335; ANX; 4;
 E; PS00223; ANNEKIN; 3.
 n; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 R 302 302
 CE 302 AA; 33965 MW; AB9FB40934A3D007 CRC64;
 ch 86.9%; Score 1390; DB 11; Length 302;
 1 Similarity 92.0%; Pred. No. 2.7e-92;
 276; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 5 LRGTVDFFGDFERADAETLRKAMKGLGTDEESITLTLTSRNSAQRQEISAAFKTLFGRL 64
 3 LRGTVDFFGDFGRADAELVRKAMKGLGTDEESITLTLTSRNSAQRQEISAAFKTLFGRL 62
 65 LLDLKSSELTKGPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 124
 63 LVNDMSKSELTKGPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 122
 25 IKQAYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGE 184
 23 IKQAYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGE 182
 85 LKNGTDEEKITITIGTRSVSHLRKVFQKMTISGQFIEETIDRETSGNLEQLLAVVKSIR 244
 83 LKNGTDEEKITITIGTRSVSHLRKVFQKMTISGQFIEETIDRETSGNLEQLLAVVKSIR 242
 45 RSIPAYLAETLYYAMKAGGTDHDLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 304
 43 RSIPAYLAETLYYAMKAGGTDHDLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 302

PRELIMINARY; PRT; 318 AA.

-2003 (TrEMBLrel; 25, Created)
 -2003 (TrEMBLrel; 25, Last sequence update)
 -2003 (TrEMBLrel; 25, Last annotation update)
 etical protein (Fragment)
 s laevis (African clawed frog).
 ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Whole;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Whole;
 RC Klein S., Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054175; AAH54175.1; -;
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 318 AA; 35590 MW; 9ED56781D9916D00 CRC64;
 Query Match 78.4%; Score 1255; DB 13; Length 318;
 Best Local Similarity 75.6%; Pred. No. 1.6e-82;
 Matches 238; Conservative 44; Mismatches 33; Indels 0; Gaps 0;
 QY 6 RGTVDFFGDFERADAETLRKAMKGLGTDEESITLTLTSRNSAQRQEISAAFKTLFGRL 65
 DB 3 RGTVDFFGDFGRADAELVRKAMKGLGTDEESITLTLTSRNSAQRQEISAAFKTLFGRL 62
 QY 66 LDDLKSSELTKGPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
 DB 63 VDLKSEISGKPEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 122
 QY 126 KQVYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGE 185
 DB 123 KQVYEEYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGE 182
 QY 186 KNGTDEEKITITIGTRSVSHLRKVFQKMTISGQFIEETIDRETSGNLEQLLAVVKSIR 245
 DB 183 KNGTDEEKITITIGTRSVSHLRKVFQKMTISGQFIEETIDRETSGNLEQLLAVVKSIR 242
 QY 246 SIPAYLAETLYYAMKAGGTDHDLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 305
 DB 243 SIPEYLAETLYYAMKAGGTDHDLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGD 302
 QY 306 GYKKAALLLCGGDD 320
 DB 303 GYRNALLLCGGDD 317

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RESULT 5
Q7ZY99 PRELIMINARY; PRT; 351 AA.
AC Q7ZY99;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment)
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043882; AAH43882.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR Hypothetical protein.
KW NON_TER
FT
SQ SEQUENCE 351 AA; 39321 MW; FF71B665A38CA8AE CRC64;

Query Match 78.4%; Score 1255; DB 13; Length 351;
Best Local Similarity 75.6%; Pred. No. 1.8e-82;
Matches 238; Conservative 44; Mismatches 33; Indels 0; Gaps 0;

QY 6 RGTVDFFGDERADAETLRKAMKGLGTDESIILTLTSSNAQROEISAAFKTLFGKDL 65
Db 36 RGTIDFFGFRKANDAEALRKAMKGLGTDEDAIKILISRNAQROEIDVAYKTLFGKDL 95
QY 66 LDDLKSELTKGPEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 96 VDDLKSEISGKENLIVALTMTPSALYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 155
QY 126 KQVYEEVGSLEDDVGGTSGYQRMVLVLLQANRDPDAGIDEAQVQDAQALFQAGEL 185
Db 156 KQVYQEQYEITLEDITGDTGYFQRMVLVLLQGNRDPDSKYNDSLVEQDAQDLFKAGEV 215
QY 186 KWTDEEKFTITFGTRSVSHLRKVFQKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 245
Db 216 KWTDEEKFTITLGRSVSHLRKVFQKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 275
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 305
Db 276 SIPEYLAETLYHAIKAGTDDCTLLIRVWVSRSEIDLLOIKERKNFGKSLHAMIQGDTS 335
QY 306 GDYKALLLCCGEDD 320
Db 336 GDYRNALLLCCGGDD 350

RESULT 6
Q93445 PRELIMINARY; PRT; 317 AA.
AC Q93445;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin max2.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

RESULT 7
Q803A1 PRELIMINARY; PRT; 317 AA.
AC Q803A1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

OC Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025617; PubMed=9809745;
RA Osterloh D., Wittbrodt J., Gerke V.;
RT "Characterization and developmentally regulated expression of four
RT annexins in the killifish medaka.";
RL DNA Cell Biol. 17:835-847(1998).
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; Y11253; CA72123.1; -.
DR HSP; P17153; IALA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
KW SEQUENCE 317 AA; 34765 MW; AFD618681BAFF0FE CRC64;

Query Match 65.8%; Score 1052; DB 13; Length 317;
Best Local Similarity 64.8%; Pred. No. 7e-68;
Matches 204; Conservative 48; Mismatches 61; Indels 2; Gaps 1;

QY 6 RGTVDFFGDERADAETLRKAMKGLGTDESIILTLTSSNAQROEISAAFKTLFGKDL 65
Db 4 KGTVKAANFKASADAELVHKAMKGLGTDEDAIQLQVCARSNAQROEIKATYKTLFGKDL 63
QY 66 LDDLKSELTKGPEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 64 INELKSELGGKFETLIVALTMTPTAYDVSVLUNAIGAGTDEKVLVEILASRTPEELRAI 123
QY 126 KQVYEEVGSLEDDVGGTSGYQRMVLVLLQANRDPDAGIDEAQVQDAQALFQAGEL 185
Db 124 IAYRKYEDADLEEDICDTSGHFRLLVLLQANR--QTGVQGGDENDAQVLFKAGEQ 181
QY 186 KWTDEEKFTITFGTRSVSHLRKVFQKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 245
Db 182 KFGTDEQTFVLLGNRSQAHLRKVFQKMTISGFOIETIDRETSGNLEQLLLAVVKSIR 241
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 305
Db 242 SVPAFYAETLYNAMKAGTDDHTLIRVWVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 301
QY 306 GDYKALLLCCGEDD 320
Db 302 GDYRNALLLCCGGDD 316

RESULT 8
Q803A1 PRELIMINARY; PRT; 317 AA.
AC Q803A1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

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BC046873; AAH46873.1; --
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
PRO; IPR001464; Annexin.
PF00191; annexin; 4.
S; PR00196; ANNEXIN.
N; PD000143; Annexin; 4.
SM00335; ANX; 4.
TE; PS00223; ANNEXIN; 4.
E; PS00223; ANNEXIN; 4.
E; PS00223; ANNEXIN; 4.
NCE 317 AA; 35060 MW; B33DA22F3DFBBD5 CRC64;
ch 64.2%; Score 1027; DB 13; Length 317;
l Similarity 64.4%; Pred. No. 4.5e-66;
203; Conservative 49; Mismatches 61; Indels 2; Gaps 1;
6 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAFAKTLFGDRL 65
4 RGTVPQSGFNANSDAEVLTKAMKGLGTDEDSILQLITKESNGORPEIKAAKTLHGKDL 63
66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAI 125
64 VNDLKSELGKGFEDLIVALTMTPTIIEVETCLRNAIKAGTDEKVLIEILASRSPNEVNEI 123
126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLVLLQANRPDPDAGIDEAQAQALFQAGEL 185
124 KSSYKREHDKLEEDVTGDTGGHFERMLVLLQASR--QQGIQESLIQSDAALFAAGEQ 181
186 KWTGDEBEKFTITFGTRSVSHLRKVFQKYMITSQFQIBETIDRETSGNLEQLLAVVKSIR 245
182 KYGTDEGQFITILGNRSNAHLRVFVEYRKLSGFEIEESIQRETSGSLQILLAVVKAR 241
246 SIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLINIRKFRKPNFATSLYSMIKGDTS 305
42 SVPGYPADSLYAAMKAGTDDQTLIRIMVTRSEVLLDIRAEFRKFRATSLHKMIQSDTS 301
06 GDYKALLILCGDD 320
02 GDYKRTLLILCGDD 316
PRELIMINARY; PRT; 317 AA.
-2003 (TrEMBLrel. 24, Created)
-2003 (TrEMBLrel. 24, Last sequence update)
-2003 (TrEMBLrel. 25, Last annotation update)
n 5.
danio rerio (Zebrafish) (Danio rerio).
ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
pterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
idae; Danio.
axID=7955;
CE FROM N.A.
S.A.; Olson E.S.; Halpern M.B.;
ebrafish Annexin (Gene Family);
Res. 0:0-0(2003).
AY178799; AAC20273.1; --
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
; SM00335; ANX; 4.
E; PS00223; ANNEXIN; 4.
E; PS00223; ANNEXIN; 4.
NCE 317 AA; 35057 MW; 082CF83C9F29D6AF CRC64;
ch 64.18; Score 1025; DB 13; Length 317;
l Similarity 64.4%; Pred. No. 6.2e-66;
203; Conservative 49; Mismatches 61; Indels 2; Gaps 1;

QY 6 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAFAKTLFGDRL 65
Db 4 RGTVPQSGFNANSDAEVLTKAMKGLGTDEDSILQLITKESNGORPEIKAAKTLHGKDL 63
QY 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAI 125
Db 64 VNDLKSELGKGFEDLIVALTMTPTIIEVETCLRNAIKAGTDEKVLIEILASRSPNEVNEI 123
QY 126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLVLLQANRPDPDAGIDEAQAQALFQAGEL 185
Db 124 KSSYKREHDKLEEDVTGDTGGHFERMLVLLQASR--QQGIQESLIQSDAALFAAGEQ 181
QY 186 KWTGDEBEKFTITFGTRSVSHLRKVFQKYMITSQFQIBETIDRETSGNLEQLLAVVKSIR 245
Db 182 KYGTDEGQFITILGNRSNAHLRVFVEYRKLSGFEIEESIQRETSGSLQILLAVVKAR 241
QY 246 SIPAYLAETLYAMKAGTDDHTLIRVMVSRSEIDLINIRKFRKPNFATSLYSMIKGDTS 305
Db 242 SVPGYPADSLYAAMKAGTDDQTLIRIMVTRSEVLLDIRAEFRKFRATSLHKMIQSDTS 301
QY 306 GDYKALLILCGDD 320
Db 302 GDYKRTLLILCGDD 316
RESULT 9
QCEXO PRELIMINARY; PRT; 476 AA.
AC QCEXO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK010342; BAC25291.1; --
DR MGD; MGI:88255; Auxa6
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 6.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 6.
DR SMART; SM00335; ANX; 5.
DR PROSITE; PS00223; ANNEXIN; 5.
SQ SEQUENCE 476 AA; 53669 MW; 9390C5B5E6653D24 CRC64;
Query Match 58.9%; Score 942; DB 11; Length 476;
Best local similarity 59.4%; Pred. No. 1.1e-59;
Matches 187; Conservative 48; Mismatches 80; Indels 0; Gaps 0;
QY 6 RGTVDPPGDERADAETLRKAMKGLGTDEESILTLTSRSNAQROEISAFAKTLFGDRL 65
Db 11 RGSVHDFPEFDANQDAEALYTKMGFGSKDESILEITSRNQROEIQNYKSLYKDL 70
QY 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAI 125
Db 71 IEDLKVELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPPELRAI 125
QY 126 KQVVEEYSGSLEDVVGDTSGYYQYRMVLVLLQANRPDPDAGIDEAQAQALFQAGEL 185

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Db 131 VAAKDAYERDLESIIIGTSGHFKMLVLLQGTRENDVVSDELVDQDLYEAGEL 190
Qy 186 KWTGDEEKFITFTGTRSVSHLRKVPDKYMTISGQIBETIDRETSGNLEQLLAVKVSIR 245
Db 191 KWTGDEAQFIYILGNRSKQHLRLVFEYKTKTGPKPIEASIREELSGDFEKLMLAVVKCIR 250
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMSVSEIDLNFIRKFNKFNATSLYSIMKGDTS 305
Db 251 STPEYFAERLFPKAMKGLGTRNTLIRIMVSRSELDMLDIRIFRTKYEKSILYSIMKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 10
Q99JX6 PRELIMINARY; PRT; 667 AA.
AC Q99JX6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -!- SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
DR EMBL; BC005595; AA005595.1; -.
DR HSP; P79134; IAVC.
DR MGD; MGI:88255; Anxa6.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 667 AA; 75260 MW; 363088A2A55CF34 CRC64;

Query Match 58.9%; Score 942; DB 11; Length 667;
Best Local Similarity 59.4%; Pred. No. 1.8e-59;
Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

Qy 6 RGVTDPPGDERADAEITLRKAMKGLGTDDEESILTLTSSNAQROEISAAFKTLFGRDL 65
Db 11 RGSVHDFPFDDANQDAEALYTAMKFGSDKESILELITSSNKQROEIQSYKSLYGKDL 70
Qy 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELRAI 125
Db 71 IEDLKVELTKGFERLIVLMRPLAYCDAKEIKDAISIGTGDEKCLIEILASRTNEQMHL 130
Qy 126 KQVVEEYSGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 131 VAAKDAYERDLESIIIGTSGHFKMLVLLQGTRENDVVSDELVDQDLYEAGEL 190
Qy 186 KWTGDEEKFITFTGTRSVSHLRKVPDKYMTISGQIBETIDRETSGNLEQLLAVKVSIR 245
Db 191 KWTGDEAQFIYILGNRSKQHLRLVFEYKTKTGPKPIEASIREELSGDFEKLMLAVVKCIR 250
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMSVSEIDLNFIRKFNKFNATSLYSIMKGDTS 305
Db 251 STPEYFAERLFPKAMKGLGTRNTLIRIMVSRSELDMLDIRIFRTKYEKSILYSIMKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 12
Q7TMN7

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Db 251 STPEYFAERLFPKAMKGLGTRNTLIRIMVSRSELDMLDIRIFRTKYEKSILYSIMKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 11
Q8BSS4 PRELIMINARY; PRT; 673 AA.
AC Q8BSS4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Annexin A6.
GN ANXA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA The FANTOM Consortium,
RC STRAIN=C57BL/6J; TISSUE=Body;
RC MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030728; BAC27101.1; -.
DR MGD; MGI:88255; Anxa6.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PRO0196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
SQ SEQUENCE 673 AA; 75885 MW; DCC5FC56CDB88809 CRC64;

Query Match 58.8%; Score 940; DB 11; Length 673;
Best Local Similarity 59.4%; Pred. No. 2.5e-59;
Matches 187; Conservative 48; Mismatches 80; Indels 0; Gaps 0;

Qy 6 RGVTDPPGDERADAEITLRKAMKGLGTDDEESILTLTSSNAQROEISAAFKTLFGRDL 65
Db 11 RGSVHDFPFDDANQDAEALYTAMKFGSDKESILELITSSNKQROEIQSYKSLYGKDL 70
Qy 66 LDDLKSELTKGFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELRAI 125
Db 71 IEDLKVELTKGFERLIVLMRPLAYCDAKEIKDAISIGTGDEKCLIEILASRTNEQMHL 130
Qy 126 KQVVEEYSGSSLEDDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 131 VAAKDAYERDLESIIIGTSGHFKMLVLLQGTRENDVVSDELVDQDLYEAGEL 190
Qy 186 KWTGDEEKFITFTGTRSVSHLRKVPDKYMTISGQIBETIDRETSGNLEQLLAVKVSIR 245
Db 191 KWTGDEAQFIYILGNRSKQHLRLVFEYKTKTGPKPIEASIREELSGDFEKLMLAVVKCIR 250
Qy 246 SIPAYLAETLYYAMKAGTDDHTLIRVMSVSEIDLNFIRKFNKFNATSLYSIMKGDTS 305
Db 251 STPEYFAERLFPKAMKGLGTRNTLIRIMVSRSELDMLDIRIFRTKYEKSILYSIMKNDTS 310
Qy 306 GDYKALLLLCGEDD 320
Db 311 GEYKALLKLCGGDD 325

RESULT 12
Q7TMN7

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7 PRELIMINARY; PRT; 319 AA.
AC 07T391
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053208; AAH53208.1; -;
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 51425 MW; E4F7F527E30F6DD7 CRC64;

Query Match 57.2%; Score 915; DB 13; Length 483;
Best Local Similarity 57.5%; Pred. No. 9.8e-58;
Matches 181; Conservative 53; Mismatches 81; Indels 0; Gaps 0;
Qy 6 RGVTPDFGDERADAEIIRKAMKGLGTDDESIITLLTSRSNAQRQEIISAFKTLFGDRL 65
Db 169 RGSIQDFPGADPLRDAEVLKAMKGFDTDEQALINLLGSRNQRQVPELVSYKTAYGKDL 228
Qy 66 LDCLKSELTKPKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 229 IKDLKSELGNFEKVLAMKLPKPSQDAYELKKAIGAGTDEACLEILASRSNAEIREI 289
Qy 126 KQVVEEYGSLEDDVVGDTSGYQYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 289 NOVFKAEKKSLDEDAISGDTSGHFRLLVSLAQNRESENVDISIAKTDQAALYQAGEN 348
Qy 186 KWGTDEKFTITPGTSVSHLRKVKFYKMTISQFIEETIDRETSGNLEQLLAVKSIK 245
Db 349 KLGTDSKFNAILCARSKAHLRAVFNEYQHMCRDIEKSIEREMSGDLGSLAVKCIK 408
Qy 246 SIPAYLAETLYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFRKNPATSLYSIMIKGDT 305
Db 409 NTPAYFAERLHKAMKAGTKDRTLIRIMVTRSEVMDLDIRQYAKNYGKSLYTAISGDT 468
Qy 306 GDYKALLLCGGDD 320
Db 469 GDYKLLKLCGGSD 483

Qy 7 GTVTDFPGDERADAEIIRKAMKGLGTDDESIITLLTSRSNAQRQEIISAFKTLFGDRL 66
Db 6 GTVKAASGFNATDAQTLRKMKGITDEDAICILAYRTAQOEIRSAKSTIGEDLI 65
Qy 67 DLKSELTKPKELIVALKMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 126
Db 66 EDLKSELSSNFQVILGLMPTVLVDYQELRRAMKAGTDEGCLEILASRTPEELRRIN 125
Qy 27 QVVEEYGSLEDDVVGDTSGYQYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 186
Db 26 QTYQQQYGRLEEDICDSTFMFQVRLVLSAAGRDEGNLDDALMKQDAQALYEAGEKR 185
Qy 87 WGTDEKFTITPGTSVSHLRKVKFYKMTISQFIEETIDRETSGNLEQLLAVKSIK 246
Db 86 WGTDEKFTITPGTSVSHLRKVKFYKMTISQFIEETIDRETSGNLEQLLAVKSIK 245
Qy 47 IPAYLAETLYAMKAGTDDHTLIRVWVSRSIDLFNIRKEFRKNPATSLYSIMIKGDT 306
Db 46 KPSYFAERLHKAMKAGTKDRTLIRIMVTRSEVMDLDIRQYAKNYGKSLYTAISGDT 305
Qy 07 DYKALLLCGGDD 320
Db 06 DYKVLILLCGGD 319

cterization and developmentally regulated expression of four
 ns in the killifish medaka."
 ll Biol. 17:835-847(1998).
 MAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
 LCTUM AND PHOSPHOLIPID (BY SIMILARITY).
 MILARITY: BELONGS TO THE ANNEXIN FAMILY.
 ILARITY: CONTAINS 4 ANNEXIN REPEATS.
 Y11255; CAA72125.1; -
 P79134; IAVC.
 :0005509; F:calcium ion binding; IEA.
 ro; IPR001464; F:calcium-dependent phospholipid binding; IEA.
 ro; IPR006031; XYPX.
 PF00191; annexin; 4.
 PF02162; XYPX; 15.
 ; PR00196; ANNEXIN.
 ; PD000143; ANNEXIN; 4.
 SM00335; ANX; 4.
 E; PS00223; ANNEXIN; 4.
 n; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 CE 508 AA; 53051 MW; 3C6728D475CAE430 CRC64;
 ch 54.1%; Score 866; DB 13; Length 508;
 l Similarity 55.6%; Pred. No. 3.6e-54;
 175; Conservative 51; Mismatches 89; Indels 0; Gaps 0;
 6 RGTVPDPPGDERADAETLRKAMKGLTDEESILTLTSSNAQROEISAAPKTLFGDRL 65
 94 RGSIKDFPGADPLRDVEVLKAMKGFDTDEKAIIELLGNRTNKQRPVPLAAAYKTYGKOL 253
 66 LDLSKELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPSELRAI 125
 54 FRLKSELTGNFEDLVVAMLKTFQFDASLRAIKAGTDEACLEIILSSRSNAIIEI 313
 26 KQYVEEYGSLEDDVVGDTSGYQYRMVLLVLANRDPDAGIDEAQVEQDAQALFOAGEL 185
 14 NKVYKAEYKGLTDESSDTSGHFRLLVSLCQGNDRERETVDISLAKDAQKLYAAGEN 373
 86 KWTDEKFTITIGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIR 245
 74 KVTDESQFNAILCARSKPHLRVFEYQYQMGCKEIKSICRETSGNLEDDGMVAVVKCIK 433
 46 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDILFNIRKEFRKNFATSLYSIMIKGDT 305
 34 NTPAYFAERLHKAMGAGTKDRTLIRVMVSRSELDMLDIRQVLRFGKSLYTHISGDT 493
 06 GDYKALLLCCGEDD 320
 94 GDYKLLKLCGSSD 508
 PRELIMINARY; PRT; 485 AA.
 -2003 (TrEMBLrel. 24, Created)
 -2003 (TrEMBLrel. 24, Last sequence update)
 -2003 (TrEMBLrel. 25, Last annotation update)
 n 11b.
 danio rerio (zebrafish) (Danio rerio).
 ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 pterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 idae; Danio.
 axID=7955;
 CE FROM N.A.
 S.A.; Olson E.S.; Halpern M.E.;
 ebrafish Annexin (Gene Family).";
 Res. 0:0-0(2003).
 AY178802; AAC20276.1; -
 :0005509; F:calcium ion binding; IEA.
 :0005544; F:calcium-dependent phospholipid binding; IEA.

InterPro; IPR001464; Annexin.
 InterPro; IPR006031; XYPX.
 Pfam; PF00191; annexin; 4.
 Pfam; PF02162; XYPX; 9.
 PRINTS; PR00196; ANNEXIN.
 ProDom; PD000143; ANNEXIN.
 SMART; SM00335; ANX; 4.
 PROSITE; PS00223; ANNEXIN; 4.
 SEQUENCE 485 AA; 51461 MW; 59D4EE05C4FA253C CRC64;
 Query Match 53.9%; Score 862; DB 13; Length 485;
 Best Local Similarity 54.9%; Pred. No. 6.6e-54;
 Matches 173; Conservative 53; Mismatches 89; Indels 0; Gaps 0;
 QY 6 RGTVPDPPGDERADAETLRKAMKGLTDEESILTLTSSNAQROEISAAPKTLFGDRL 65
 DB 171 RGTIKDFPGADPLRDVEVLKAMKGFDTDEKAIIELLGSRSNKQRPVPLAAAYKTYGKOL 230
 QY 66 LDLSKELTGKFEKLI VALMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPSELRAI 125
 DB 231 VRDLKSELTGHPFELVLA MLKSPAQFDASECKEATISGAGTDEACLEIILSSRSNAIIEI 290
 QY 126 KQYVEEYGSLEDDVVGDTSGYQYRMVLLVLANRDPDAGIDEAQVEQDAQALFOAGEL 185
 DB 291 NRIYKAEYKGLTDESSDTSGHFRLLVSLCQGNDRERETVDISMAKDAQKLYHAGEN 350
 QY 186 KWTDEKFTITIGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAVVKSIR 245
 DB 351 KVTDESQFNAILCARSKPHLRVFEYQYQMGCKEIKSICRETSGNLEDDGMVAVVKCIK 410
 QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDILFNIRKEFRKNFATSLYSIMIKGDT 305
 DB 411 NTPAYFAERLHKAMGAGTKDRTLIRVMVSRSELDMLDIRQVLRFGKSLYTHISGDT 470
 QY 306 GDYKALLLCCGEDD 320
 DB 471 GDYKLLKLCGSSD 485
 RESULT 18
 Q90X16 PRELIMINARY; PRT; 321 AA.
 AC Q90X16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Annexin 4.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seville R.A., Nijjar S., Barnett M.W., Jones E.A.;
 RT "Annexin 4 (Xanx-4) has a role in the development of the pronephric
 RT tubules in Xenopus laevis."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
 CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
 DR EMBL; AY039235; AAK83461.1; -
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; ANNEXIN; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
 Repeat.


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:0005544; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
SM00335; ANX; 4.
E; PS00223; ANNEXIN; 4.
etical protein.
CE 321 AA; 72F81AD1E753B29D CRC64;
ch 53.4%; Score 855; DB 13; Length 321;
l Similarity 53.2%; Pred. No. 1.2e-53;
166; Conservative 62; Mismatches 84; Indels 0; Gaps 0;
6 RGVTVDPFGDERADAETLRKAMKGLGTDEESILTLLTSRSNAQROEISAAFKTLFGRDL 65
7 RGVTVASGPKPDQAQIYNAMKAGTNEATIEILAHRTIAQOKKEAFKLSVGKL 66
66 LDLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRAL 125
67 MDCLKSELTKGNFVKVVGMLMPAAVYDAHELNAIKAGTTEACLDILASRSNABIKI 126
26 KQVVEEYGSLEDDVVGDTSGYQYRMVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 195
27 VAAVYKKEHDKSLEDDICGDTSGMFORVLVSLLTAGRDESTKVDQAQVQDAKDIYEAGEA 186
86 KWGTDEKFTITGTRSVSHLRKVFQKYMVTISGFQIBETIDRETSGNLEQLLLAVVKSIR 245
87 RWGTVDEVKFLTVLCVRNRHLLRVFQYQKSGRDIEDSIKRENGSLEDDVFLAIVKCIK 246
46 SIPAYLAETLYAMKAGTDDHTLIRVWVSERSEIDLNFIRKFKNFATSLYSIMKIGDTS 305
47 NKFAFFAERLYKSKMGLGTTDSVLIRIMVARAEIDMLDIKAEFLKMGVTLHSFIKGDTS 306
06 GDYKALLLCCG 317
07 GDYKILLELCCG 318
PRELIMINARY; PRT; 327 AA.
-2002 (TrEMBLrel. 22, Created)
-2002 (TrEMBLrel. 22, Last sequence update)
-2003 (TrEMBLrel. 25, Last annotation update)
ar to annexin A8.
usculus (Mouse).
ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
taxID=10090;
CE FROM N.A.
ted (MAY-2002) to the EMBL/GenBank/DBJ databases.
BC030407; AAH30407.1; -.
GI:1201374; Anx8.
:0005509; F:calcium ion binding; IEA.
:0005544; F:calcium-dependent phospholipid binding; IEA.
ro; IPR001464; Annexin.
PF00191; annexin; 4.
; PR00196; ANNEXIN.
; PD000143; Annexin; 4.
SM00335; ANX; 4.
E; PS00223; ANNEXIN; 4.
CE 327 AA; 56DB9CFAFA8C2B21 CRC64;
ch 52.6%; Score 841.5; DB 11; Length 327;
al Similarity 57.8%; Pred. No. 1.1e-52;
177; Conservative 49; Mismatches 79; Indels 1; Gaps 1;
15 FDERADATLRKAMKGLGTDEESILTLLTSRSNAQROEISAAFKTLFGRDLDDLKSELT 74

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Db 21 FNPDPDAETLYKAMKIGTNEQAIIDVLTKRSNVQRQIAKSFKAQFGKDLTETLKSLS 80
QY 75 GKPEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRALIKQVVEEY 134
Db 81 GKFERLIIVAMPYPPSYSEAKELHDAKMGIGTKEGVIEILASRTKQNLREIMKAYBEDY 140
QY 135 SSILEDVVGDTSGYQYRMVLLQANRDPDAG-IDEAQVEQDAQALFOAGELKMGTDDEK 193
Db 141 STLEEDIQDGTGYLERILVCLLQGRSDVSGFVDPGLVLQDAQALHEAGEKMGTDDEK 200
QY 194 FTITGTRSVSHLRKVFQKYMVTISGFQIBETIDRETSGNLEQLLLAVVKSIRSIPAYLAE 253
Db 201 FITILCTRATHLMRVFEYEYKIANKCIEDSIKSETHSGSLEEAMLTVVKCTRVNHSYFAE 260
QY 254 TLYAMKAGTDDHTLIRVWVSERSEIDLNFIRKFKNFATSLYSIMKIGDTSYDKKALL 313
Db 261 RLYAMKAGTDDHTLIRVWVSERSEIDLNLINGQFKMGKTLSSMIMADTSGYKTKALL 320
QY 314 LIGGED 319
Db 321 NLVGTD 326
RESULT 22
Q95L54 PRELIMINARY; PRT; 327 AA.
AC Q95L54;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Annexin VIII.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA White A.H., Wallis G.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR
CC CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
DR EMBL; AF417637; AAL13308.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
KW Repeat.
SQ SEQUENCE 327 AA; 36787 MW; 2EB178E13738CF22 CRC64;
Query Match 52.3%; Score 837.5; DB 6; Length 327;
Best Local Similarity 55.9%; Pred. No. 2.2e-52;
Matches 175; Conservative 53; Mismatches 84; Indels 1; Gaps 1;
QY 8 TVTDFGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQROEISAAFKTLFGRDLDD 67
Db 14 SVKGSHPNPDPAETLYKAMKIGTNEQAIIDVLTKRSNAQROEISAAFKTLFGRDLDD 73
QY 68 DLKSELTKGFEKLIIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIATSRTPPELRALIKQ 127
Db 74 TLKSELSGFERLIIVAMPYPPSYSEAKELHDAKMGIGTKEGVIEILASRTKQNLREIMK 133
QY 128 VYEEYGSLEDDVVGDTSGYQYRMVLLQANRDPDAG-IDEAQVEQDAQALFOAGELK 186
Db 134 AYEDYGSNLEEDIKADTSGYLERILVCLLQGRSDVSGFVDPGLVLQDAQALFOAGELK 193

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QY 187 WGTDEKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIRS 246
Db 194 CGTDEMKFTITLCTRSATHLMRVFEYEEKIANSIEDSIKSETHGSLEBAMLTIVKCTRN 253
QY 247 IPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 306
Db 254 LHGYFAERLYAMKAGTDLGTLIRNIVSRSEIDLNLKQKMYGKTLSSMIMEDTSG 313
QY 307 DYKALLLLCGED 319
Db 314 DYKNALLNLVGS 326

RESULT 23
O97529
ID O97529 PRELIMINARY; PRT; 327 AA.
AC O97529;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Annexin VIII.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng W., Tsao F.H.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF012745; AAD01508.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR SEQUENCE 327 AA; 36680 MW; 1815B77B6BE50AB7 CRC64;

Query Match 51.5%; Score 823.5; DB 6; Length 327;
Best Local Similarity 55.9%; Pred. No. 2.2e-51;
Matches 175; Conservative 48; Mismatches 89; Indels 1; Gaps 1;

QY 8 TVTDFPGFPERADAETLRKAMKGLGTDESIILTLTSRNSAQRQETSAAPKTLFGDRLD 67
Db 14 TVKGSFHPFVPAETLYKAMKGLGTDESIILTLTSRNSAQRQETSAAPKTLFGDRLD 73
QY 68 DLKSELTKGFEKLIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 127
Db 74 TLKSELGKFEKLIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 133
QY 128 VVEEYEGSSLEDDVVGDTSGYQYRMVLVLLQANRDPDAG-IDEAQVEQDAQALFOAGELK 186
Db 134 ANEEDYGGSSLEDDVVGDTSGYQYRMVLVLLQANRDPDAG-IDEAQVEQDAQALFOAGELK 193
QY 187 WGTDEKFTITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIRS 246
Db 194 CGTDEMKFTITLCTRSATHLMRVFEYEEKIANSIEDSIKSETHGSLEBAMLTIVKCTRN 253
QY 247 IPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 306
Db 254 LHGYFAERLYAMKAGTDLGTLIRNIVSRSEIDLNLKQKMYGKTLSSMIMEDTSG 313
QY 307 DYKALLLLCGED 319
Db 314 DYKNALLNLVGS 326

RESULT 24
Q8C1X9
ID Q8C1X9 PRELIMINARY; PRT; 323 AA.
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AC Q8C1X9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Annexin A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22354683; PubMed=12466851;
RC TISSUE=Kidney;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK090055; BAC41070.1; -.
DR MGD; MGI:1201378; Anxa3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
DR SEQUENCE 323 AA; 36356 MW; 9F69F57BCFAC6A85 CRC64;

Query Match 50.6%; Score 809; DB 11; Length 323;
Best Local Similarity 49.5%; Pred. No. 2.4e-50;
Matches 156; Conservative 63; Mismatches 96; Indels 0; Gaps 0;

QY 6 RGTVDTPGFERADAETLRKAMKGLGTDESIILTLTSRNSAQRQETSAAPKTLFGDRLD 65
Db 9 RGTIKDYPGFSVDAAEIRKAIKGLGTDEKTLINILTERSNAQRQETSAAPKTLFGDRLD 68
QY 66 LDDKSELTKGFEKLIVAMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
Db 69 KDDLKGLSGHFEHVWVALVTAPALFDKQLKSMKGTGDEDALEIILTLTSRQMKBI 128
QY 126 KQVVEEYEGSSLEDDVVGDTSGYQYRMVLVLLQANRDPDAGIDEAQVEQDAQALFOAGEL 185
Db 129 SQAYTVTVKSLGDDISSETSGDFPKALLTLADGRDSESLKVDEHLAKDAQILYNAGEN 188
QY 186 KWTDEEKFITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIR 245
Db 189 KWTDEEKFITFOTRSVSHLRKVDKMYTISGQIEETIDRETSGNLEQLLAVVKSIR 248
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLNFIRKEFRKNFATSLYSMIKGDTS 305
Db 249 NTPFLAERLHQAALKGAGTDEFTLIRNIVSRSEIDLNLKQKMYGKTLSSMIMEDTSG 308
QY 306 GDYKALLLLCGED 320
Db 309 GDYRTVLLKIGGED 323

RESULT 25
Q222A2
ID Q222A2 PRELIMINARY; PRT; 463 AA.
AC Q222A2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Annexin A7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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99 643 40.2 346 2 AAR06560
100 642 40.1 345 7 ADE60115

AAR06560 Human 11p
ADE60115 Human Pro

ALIGNMENTS

RESULT 1

AAP80511

ID AAP80511 standard; protein; 320 AA.

XX AAP80511;

AC 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 12-NOV-1990 (first entry)

XX Placental coagulation inhibitor.

XX Placental coagulation inhibitor; disseminated vascular coagulation;

XX thrombosis.

XX Homo sapiens.

XX EP279459-A.

XX 24-AUG-1998.

XX 19-FEB-1998; 88EP-00102468.

XX 20-FEB-1987; 87JP-00037227.

XX 23-JUL-1987; 87JP-00184428.

XX (KOMA) KOMA CO LTD.

XX Saino Y, Iwasaki A, Suda M;

XX WPI; 1988-236733/34.

XX N-PSDB; AAN81113.

Recombinant placental coagulation inhibitor - useful for the prevention and treatment of thromboses or disseminated intravascular coagulation.

XX Disclosure; Page 7; 31pp; English.

XX This polypeptide exhibits strong anticoagulant activities and is useful

XX for the treatment and prevention of e.g. thrombosis or disseminated

XX intravascular coagulation in the brain, heart and peripheral blood

XX vessels, such as cerebral and myocardial infarction. It has no

XX antigenicity against man and can be produced in large amts. using

XX recombinant methods. (Updated on 10-MAR-2003 to add missing CS field.)

XX (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to

XX correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 320 AA;

Query Match 100.0%; Score 1600; DB 1; Length 320;

Best Local Similarity 100.0%; Pred. No. 1.3e-134;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOVLRGVTVDFPGFDERADAETLRKAMKGGTDEESITLTLTSRSNAOROEISAAPKTL 60

DB 1 MAOVLRGVTVDFPGFDERADAETLRKAMKGGTDEESITLTLTSRSNAOROEISAAPKTL 60

QY 61 FGRDLDDKSELNGKFEKTLVALMKPSRLYDAVELKHALKGAGTNEKVLFEIISRTPE 120

DB 61 FGRDLDDKSELNGKFEKTLVALMKPSRLYDAVELKHALKGAGTNEKVLFEIISRTPE 120

QY 121 ELRAIKQYEEYSGSSLEDVVGDTSGYGYQMLVVLQANDPDAGIDEADEVDAQALF 180

DB 121 ELRAIKQYEEYSGSSLEDVVGDTSGYGYQMLVVLQANDPDAGIDEADEVDAQALF 180

QY 181 QAGELKMGTDSEKFTITIGTNSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 240

DB 181 QAGELKMGTDSEKFTITIGTNSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLAV 240

QY 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEKRFATSIYSMI 300

DB 241 VKSIRSIPIAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKEKRFATSIYSMI 300

QY 301 KGDTSGDYKKALLLLCGEDD 320

DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 2

AAP91953

ID AAP91953 standard; protein; 320 AA.

XX AAP91953;

XX 24-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 10-MAR-2003 (revised)

XX 30-JUL-1989 (first entry)

XX Vascular anti-coagulating protein-alpha.

XX Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.

XX Homo sapiens.

XX Mus musculus.

XX Chimeric.

XX DE3810331-A.

XX 05-OCT-1989.

XX 26-MAR-1988; 88DE-03810331.

XX 26-MAR-1988; 88DE-03810331.

XX (BOEH) BOEHRINGER INGELHEIM.

XX Gunther A;

XX WPI; 1989-293724/41.

XX N-PSDB; AAN91353.

Monoclonal antibodies to vascular anti-coagulating proteins - and hybridomas producing such antibodies.

XX Disclosure; Fig 1; 11pp; German.

XX This vascular anti-coagulating protein (VAC)-alpha is used in the

XX preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected

XX into a host animal, in conjugation with eg keyhole limpet haemocyanin,

XX and the B-cells from immunised hosts are then fused with myeloma cells.

XX The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-

XX alpha. Abs can be used as immunoassay reagents to detect VAC proteins, as

XX affinity ligands for protein purification, and as medicaments for binding

XX and/or neutralising VAC proteins in vivo. See also AAN91354 and BP-

XX 181465. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-

XX MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS

XX field)

XX Sequence 320 AA;

Query Match 100.0%; Score 1600; DB 1; Length 320;

Best Local Similarity 100.0%; Pred. No. 1.3e-134;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOVLRGVTVDFPGFDERADAETLRKAMKGGTDEESITLTLTSRSNAOROEISAAPKTL 60

DB 1 MAOVLRGVTVDFPGFDERADAETLRKAMKGGTDEESITLTLTSRSNAOROEISAAPKTL 60

QY 61 FGRLDLDLKSFLTGKEFKLIVALKMPSRLYDAVELKALKAGAGTNEKVLTEIIASRTPE 120
 DB 61 FGRLDLDLKSFLTGKEFKLIVALKMPSRLYDAVELKALKAGAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQYEEERYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 DB 121 ELRAIKQYEEERYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVFCKMTISGFOIERTIDRETSQNLLEQLLAV 240
 DB 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVFCKMTISGFOIERTIDRETSQNLLEQLLAV 240
 QY 241 VKSIRSIIPAYLAETLYYAMKAGAGTDHDLIRVWVSRSSEIDLFNIRKFRKPFATSLYSMT 300
 DB 241 VKSIRSIIPAYLAETLYYAMKAGAGTDHDLIRVWVSRSSEIDLFNIRKFRKPFATSLYSMT 300
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 3

AA13082
 ID AA13082 standard; protein; 320 AA.

AC AA13082;
 XX

DT 25-MAR-2003 (revised)
 DT 30-SEP-1991 (first entry)

DE PAP-I.

KW Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;
 KM gla-domain; VKDP.

XX Homo sapiens.

XX MO9109953-A.

PD 11-JUL-1991.

PF 29-DEC-1989; 89US-00459082.

PR 29-DEC-1989; 89US-00459082.

PA (ZYMO) ZYMOGENETICS INC.

PI Foster DC;

XX WPI, 1991-222905/30.

DR N-PSDB; AAQ12679.

PT Recombinant prodn. of hybrid phospholipid-binding proteins - comprising
 PT lipocortin phospholipid-binding domain and vitamin-K-dependent protein.

PS Disclosure; fig 7; 5pp; English.

XX This sequence, or a fragment of it, is used in the construction of hybrid
 CC phospholipid-binding proteins (PBP) comprising at least one lipocortin
 CC domainless vitamin K-dependent protein, e.g. of PAP-I, joined to a gla-
 CC protein C. See AAQ12680-81 for such examples. See also AAQ12678-81.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 320 AA;

QY Query Match 100.0%; Score 1600; DB 2; Length 320;
 DB Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAQVLRGTVDPPFDERADAEFLRKAMKGLGTDEESTLTLTSSRNAQROEISAAPFTL 60
 1 MAQVLRGTVDPPFDERADAEFLRKAMKGLGTDEESTLTLTSSRNAQROEISAAPFTL 60

QY 61 FGRLDLDLKSFLTGKEFKLIVALKMPSRLYDAVELKALKAGAGTNEKVLTEIIASRTPE 120
 DB 61 FGRLDLDLKSFLTGKEFKLIVALKMPSRLYDAVELKALKAGAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQYEEERYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 DB 121 ELRAIKQYEEERYSGSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEODQAALF 180
 QY 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVFCKMTISGFOIERTIDRETSQNLLEQLLAV 240
 DB 181 QAGELKMGTDDEKFTITIGTRSVSHLRKVFCKMTISGFOIERTIDRETSQNLLEQLLAV 240
 QY 241 VKSIRSIIPAYLAETLYYAMKAGAGTDHDLIRVWVSRSSEIDLFNIRKFRKPFATSLYSMT 300
 DB 241 VKSIRSIIPAYLAETLYYAMKAGAGTDHDLIRVWVSRSSEIDLFNIRKFRKPFATSLYSMT 300
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 4

AA13923
 ID AA13923 standard; protein; 320 AA.

AC AA13923;
 XX

DT 13-JUL-1999 (first entry)

DE S65T GFP variant/hannexin V protein.

KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 KM fluorescent intensity; anionic phospholipid binding affinity;
 KM asymmetric distribution; plasma membrane phospholipid;
 KM apoptotic cell detection.

XX Aequorea victoria.

OS Homo sapiens.

OS Synthetic.

XX MO919470-A2.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US021444.

PR 09-OCT-1997; 97US-00948276.

PA (REGC) UNIV CALIFORNIA.

PI Ernst JD;

XX WPI, 1999-277634/23.

PT Bifunctional fusion protein useful for the detection of apoptotic cel
 PT Claim 2; Page 14-15; 23pp; English.

XX This sequence represents an example of a protein of the invention. The
 CC proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties pro
 CC greater or equal fluorescent intensity and anionic phospholipid bindi
 CC affinity, respectively, than do the corresponding unfused GFP and ann
 CC asymmetric distribution of plasma membrane phospholipids, which result
 CC in exposure of anionic phospholipids on the extracellular leaflet of t
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microsc
 CC fluorescence properties that do not change upon binding annexin, with
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenchin
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholip

CC	membranes	Sequence 320 AA:	100.0%;	Score 1600;	DB 2;	Length 320;
XX	XX	Query Match	100.0%;	Pred. No. 1.3e-134;	Indels 0;	Gaps
XX	XX	Best Local Similarity	100.0%;	Mismatches 0;	Indels 0;	Gaps
XX	XX	Matches 320;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	QY	1 MAQVLRGTVNDFPFEDRRAAEITLRKMGKGTDEESITLTLSRSNAQROEISAAFKTL				60
Db	Db	1 MAQVLRGTVNDFPFEDRRAAEITLRKMGKGTDEESITLTLSRSNAQROEISAAFKTL				60
QY	QY	61 FGRRLDLDLKSGLGKPEKTLVALMKPSRLYDAEYELKHALKGATNEKVLTEIIASRTPE				12
Db	Db	61 FGRRLDLDLKSGLGKPEKTLVALMKPSRLYDAEYELKHALKGATNEKVLTEIIASRTPE				12
QY	QY	121 ELRAIKQYEEYSGSSLEDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF				16
Db	Db	121 ELRAIKQYEEYSGSSLEDVVGDTSGYQRMVLVLLQANRPDAGIDEAQVEQDAQALF				16
QY	QY	181 QAGELKMGTDEEKFTITIGTRSVSHLRKVPDKWTISGFOIEETIDETSGNLQQLLAV				2
Db	Db	181 QAGELKMGTDEEKFTITIGTRSVSHLRKVPDKWTISGFOIEETIDETSGNLQQLLAV				2
QY	QY	241 VKSIRSPAYIAETLYYAMKAGAGTDHLLIRVMSRSITDLPNIRKEPRKVFATLSMI				3
Db	Db	241 VKSIRSPAYIAETLYYAMKAGAGTDHLLIRVMSRSITDLPNIRKEPRKVFATLSMI				3
QY	QY	301 KGDTSGDYKKALLLCCGDD 320				
Db	Db	301 KGDTSGDYKKALLLCCGDD 320				
RESULT 5	AA84788	AA84788 standard; peptide; 320 AA.				
ID	AA84788	08-AUG-2000 (first entry)				
AC	AA84788;					
XX	XX	Amino acid sequence of annexin V.				
XX	XX	Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;				
XX	XX	coating; thrombogenic biomaterial; labelling compound; negative charge				
OS	OS	Unidentified.				
XX	XX	Key	Location/Qualifiers			
FT	FT	Domain	16..91			
FT	FT		/note="domain 1"			
FN	FN	FR2784106-A1.				
XX	XX	07-APR-2000.				
XX	XX	02-OCT-1998;	98FR-00012366.			
XX	XX	02-OCT-1998;	98FR-00012366.			
XX	XX	02-OCT-1998;	98FR-00012366.			
XX	XX	(COMS) COMMISSARIAT ENERGIE ATOMIQUE.				
PA	PA	(UYPA) UNIV CURIE PARIS VI P & M.				
XX	XX	Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;				
XX	XX	WPI; 2000-320664/28.				
XX	XX	Chemical structure having affinity for phospholipid comprises chemical				
XX	XX	platform comprising six residues supporting set of chemical functions				
XX	XX	that are capable of binding to phospholipid.				
XX	XX	Claim 13; Fig 6b; 63pp; French.				

The present sequence represents an annexin polypeptide. The domain of CC annexin, which may be modified, is used to construct the chemical compounds of the invention. The specification describes chemical compounds which have an affinity for a phospholipid. The chemical compounds comprise at least one chemical platform comprising six residues supporting a set of chemical functions that are capable of binding to the phospholipid and at least partly define the affinity of the structure for the phospholipid. The compounds act as phospholipid sequestrers. The compounds are useful for preparing antithrombotic, anticancer and antiinflammatory medicaments, for making coatings for thrombogenic biomaterials, and for preparing labelling compounds useful for analysing and detecting negative charges on cell surfaces and microvesicles in blood.

Sequence 320 AA:

Query Match 100.0%; Score 1600; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.3e-134;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAQVLKGTVDTPFGFDERADAEYLRKAMKGLGTDRESLITLLTSSNMOROEISAAPKTL 60
1 MAQVLKGTVDTPFGFDERADAEYLRKAMKGLGTDRESLITLLTSSNMOROEISAAPKTL 60

Qy FGRDLDLKLKSELTKFEKLIYALMKPSRLVDAYELKIALKAGTNEKVLTEIIASRTP 120
61 FGRDLDLKLKSELTKFEKLIYALMKPSRLVDAYELKIALKAGTNEKVLTEIIASRTP 120

Db FGRDLDLKLKSELTKFEKLIYALMKPSRLVDAYELKIALKAGTNEKVLTEIIASRTP 120
61 FGRDLDLKLKSELTKFEKLIYALMKPSRLVDAYELKIALKAGTNEKVLTEIIASRTP 120

Qy EIRAIKQYEEYEGSSLEDVDVGDTSYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
121 EIRAIKQYEEYEGSSLEDVDVGDTSYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 180

Db EIRAIKQYEEYEGSSLEDVDVGDTSYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 180
121 EIRAIKQYEEYEGSSLEDVDVGDTSYQYRMVLVLLQANRPDAGIDEAQVEQDAQALF 180

Qy QAGELKMGTDDEKFTTIFGTRSVSHLRKVFYDKYMTISGFQIEETIDRETSNGLQILLAV 240
181 QAGELKMGTDDEKFTTIFGTRSVSHLRKVFYDKYMTISGFQIEETIDRETSNGLQILLAV 240

Db QAGELKMGTDDEKFTTIFGTRSVSHLRKVFYDKYMTISGFQIEETIDRETSNGLQILLAV 240
181 QAGELKMGTDDEKFTTIFGTRSVSHLRKVFYDKYMTISGFQIEETIDRETSNGLQILLAV 240

Qy VASIRSIPIYLAETLYYAKKAGATDDHTLIRVWSRSEIDLIRIKREFRKNFATSLYSMT 300
241 VASIRSIPIYLAETLYYAKKAGATDDHTLIRVWSRSEIDLIRIKREFRKNFATSLYSMT 300

Db VASIRSIPIYLAETLYYAKKAGATDDHTLIRVWSRSEIDLIRIKREFRKNFATSLYSMT 300
241 VASIRSIPIYLAETLYYAKKAGATDDHTLIRVWSRSEIDLIRIKREFRKNFATSLYSMT 300

Qy KGDTSGDYKKALLLCGEDD 320
301 KGDTSGDYKKALLLCGEDD 320

Db KGDTSGDYKKALLLCGEDD 320
301 KGDTSGDYKKALLLCGEDD 320

RESULT 6
ABG31220
ID ABG31220 standard; protein; 320 AA.
XX ABG31220;
XX AC
XX DT 05-NOV-2002 (first entry)
XX DE
XX Human annexin V, containing a delta RACK binding site.
XX Human; annexin V; delta RACK; delta protein kinase C; deltaPKC;
XX VI domain; vasotrophic; cerebroprotective; deltaV1-1; deltaV1-2; RACK;
XX pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;
XX deltaV1-5; PKC; protein kinase C; signal transduction; cell growth;
XX gene expression; ion channel activity; translocation; hypoxia; stroke;
XX ischaemic damage; creatine kinase.
XX Homo sapiens.
XX OS
XX PN WO200257413-A2.
XX PD 25-JUL-2002.
XX PF 09-NOV-2001; 2001WO-US047556.
XX PR 18-JAN-2001; 2001US-0262060P.
XX PA (STPD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;
 XX
 XX
 DR WPI: 2002-599715/64.
 XX
 PT New delta protein kinase C peptide for reducing or enhancing damage to
 PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
 PT or for protecting tissue from damage due to ischemia.
 XX
 PS Claim 45; Page 64-65; 65pp; English.
 XX
 CC The invention discloses peptides comprising deltaxi-1, deltaxi-2, pseudo-
 CC delta receptors for activated C-kinase (RACK), deltaxi-5 or their
 CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
 CC signal transduction involved in a variety of cellular functions including
 CC cell growth, regulation of gene expression and ion channel activity. The
 CC localisation of different PKC isozymes to different areas of the cell in
 CC turn appears due to binding of the activated isozymes to the specific
 CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
 CC site on RACKs or the RACK-binding site on PKC are isozyme specific
 CC translocation inhibitors of PKC. The disclosed peptides are useful in
 CC activating or inhibiting translocation or function of deltaxi. The
 CC deltaxi agonists or antagonists are useful in reducing, enhancing or
 CC protecting against damage to cells or tissues due to ischemic or hypoxic
 CC event caused by stroke. Acute administration of the peptides, conjugated
 CC to a carrier peptide or a Tat-derived peptide, protected hearts against
 CC ischemic damage as shown by decreased release of creatine kinase. The
 CC data indicate that in an intact heart, inhibition of deltaxi conferred
 CC greater than 50% protection against ischemic damage. The sequence
 CC presented is human annexin V, which contains a delta RACK binding site
 XX
 SQ Sequence 320 AA;
 Query Match 100.0%; Score 1600; DB 5; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1,3e-134;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQVLRGTVTDFPFGPERADAEFLRKAMKGLGDEESITLTLRSNAQROEISAAPKTL 60
 DB 1 MAQVLRGTVTDFPFGPERADAEFLRKAMKGLGDEESITLTLRSNAQROEISAAPKTL 60
 QY 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKALKAGTNEKVLTEIIASRTPE 120
 DB 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKALKAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQNRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQNRDPDAGIDEAQVEQDAQALF 180
 QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKYFDKMTISGQIEETIDRETSGNLEQILLAV 240
 DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKYFDKMTISGQIEETIDRETSGNLEQILLAV 240
 QY 241 VKSIRSIPIAYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNFATSLYSMT 300
 DB 241 VKSIRSIPIAYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNFATSLYSMT 300
 QY 301 KGDTSGDYKAKALLLCGEDD 320
 DB 301 KGDTSGDYKAKALLLCGEDD 320

RESULT 7

AAP90053 standard; protein; 320 AA.

XX
 XX
 AC AAP90053;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-NOV-1989 (first entry)
 XX
 DE anticoagulant PP4 protein.

XX Anticoagulant; PP4 protein; thromboplasmin.
 KW Homo sapiens; (human).
 XX
 OS EP318703-A.
 XX
 PN 07-JUN-1989.
 XX
 PD 29-OCT-1988; 88EP-00118039.
 XX
 PF 03-NOV-1987; 87DE-03737239.
 XX
 PR (BEHW) BEHRINGER AG.
 XX
 PA Grundmann U, Abel KJ, Kupper H;
 XX
 DR WPI: 1989-166767/23.
 XX
 CC New DNA sequence encoding anticoagulant PP4 protein - and new recomb
 CC protein, vectors, antibodies, etc., useful therapeutically and
 CC diagnostically.
 XX
 PS Claim 1; Page 11 and Table 1; 12pp; German.
 XX
 CC Amino acid sequence of anticoagulant PP4 protein. This inhibits bloo
 CC coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to
 CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Up
 CC on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 320 AA;
 Query Match 99.8%; Score 1597; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 2,5e-134;
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps
 QY 1 MAQVLRGTVTDFPFGPERADAEFLRKAMKGLGDEESITLTLRSNAQROEISAAPKTL 60
 DB 1 MAQVLRGTVTDFPFGPERADAEFLRKAMKGLGDEESITLTLRSNAQROEISAAPKTL 60
 QY 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKALKAGTNEKVLTEIIASRTPE 120
 DB 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKALKAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQNRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVVEEYSSLEDVVDGTSYQRMVLVLLQNRDPDAGIDEAQVEQDAQALF 180
 QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKYFDKMTISGQIEETIDRETSGNLEQILLAV 240
 DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKYFDKMTISGQIEETIDRETSGNLEQILLAV 240
 QY 241 VKSIRSIPIAYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNFATSLYSMT 300
 DB 241 VKSIRSIPIAYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNFATSLYSMT 300
 QY 301 KGDTSGDYKAKALLLCGEDD 320
 DB 301 KGDTSGDYKAKALLLCGEDD 320

RESULT 8

AA92930 standard; protein; 600 AA.

XX
 XX
 AC AA92930;
 XX
 DT 25-OCT-2000 (first entry)
 DT
 XX
 DE Annexin V/urokinase fusion protein.
 XX
 KW Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protei

KW urokinase, insect cell; fibrinolysis.
 OS Unidentified.
 XX CN1247195-A.
 XX PD 15-MAR-2000.
 XX PF 12-MAR-1999; 99CN-00113524.
 XX PR 12-MAR-1999; 99CN-00113524.
 XX (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
 XX Wu X, Sun J, Yang G;
 DR WPI: 2000-413098/36.
 DR N-PSDB; AAA11241.
 XX New thrombolytic fusion protein for targeting thrombus - comprises
 PT fusion of Annexin V and urokinase.
 PS Claim 2; Page 2-4; 20pp; Chinese.
 XX Annexin V, which has high affinity for active thrombocytes, is used as a
 CC carrier molecule to build a thrombus-targeting thrombolytic fusion
 CC protein. The protein (this sequence) is the result of expression of a
 CC fusion gene comprising the Annexin V gene and a low-molecular urokinase
 CC gene, in insect cells. The Annexin V-scFv-PA-32 fusion protein, expressed
 CC in insect cell strain Tn-SB1-4, has high affinity for active thrombocytes
 CC and has the fibrinolytic activity of urokinase
 XX
 SQ Sequence 600 AA:

Query Match 99.8%; Score 1597; DB 3; Length 600;
 Best Local Similarity 99.7%; Pred. No. 5.8e-134;
 Matches 319; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPGFDERADAEITLRKAMKGLGTDSEITLTLTSRSNAQOEISAAFKTL 60
 DB 281 MAQVLRGTVDPPGFDERADAEITLRKAMKGLGTDSEITLTLTSRSNAQOEISAAFKTL 340
 QY 61 FGRDLDDLKSELGKFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 DB 341 FGRDLDDLKSELGKFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 400
 QY 121 ELRAIKQYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAQLF 180
 DB 401 ELRAIKQYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAQLF 460
 QY 181 QAGELKMGTDDEKFTITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLQQLLAV 240
 DB 461 QAGELKMGTDDEKFTITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLQQLLAV 520
 QY 241 VKSIRSIPAYLAETIIVYAMKAGTDDHTLIRVMSRSEIDLFINIKERKKNPATISYSMI 300
 DB 521 VKSIRSIPAYLAETIIVYAMKAGTDDHTLIRVMSRSEIDLFINIKERKKNPATISYSMI 580
 QY 301 KGDTSGDYKKAALLLCGEDD 320
 DB 581 KGDTSGDYKKAALLLCGEDD 600

RESULT 9
 AAP82317
 ID AAP82317 standard; protein; 320 AA.
 XX
 AC AAP82317;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-NOV-1990 (first entry)
 XX
 DE PAP-I isolated from biological fluid, used as anticoagulant.

XX PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
 KW phospholipase A2; disseminated intravascular coagulation;
 KM deep vein thrombosis.
 XX Homo sapiens.
 OS
 XX WO80805659-A.
 XX PD 11-AUG-1988.
 XX PF 05-FEB-1988; 88WO-US000340.
 XX PR 06-FEB-1987; 87US-00011762.
 XX PR 05-JUN-1987; 87US-00059355.
 XX (ZYMO) ZYMOGENETICS INC.
 PA (UNITW) UNIV WASHINGTON.
 XX Fujikawa K, Irani MH, Carter BLA;
 PI WPI: 1988-235049/33.
 DR N-PSDB; AAN82107.
 DR Human proteins having anticoagulant and antiinflammatory activity -
 PT isolated from biological fluids by anion-exchange chromatographic media.
 XX
 PS Disclosure; Page 7; 62pp; English.
 XX The protein does not contain a leader peptide sequence, indicating that
 CC PAP-I is probably not constitutively secreted. The Met residue is removed
 CC at in a post-translational event and the newly formed NH2-terminal Ala
 CC residue is blocked by acetylation. It binds to phospholipid and inhibits
 CC phospholipase A2. The protein can substitute heparin or other
 CC anticoagulants in the treatment of disseminated intravascular
 CC coagulation, deep vein thrombosis, or other disorders. It also has
 CC antiinflammatory properties. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 320 AA:

Query Match 99.8%; Score 1596; DB 1; Length 320;
 Best Local Similarity 99.7%; Pred. No. 3e-134;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPPGFDERADAEITLRKAMKGLGTDSEITLTLTSRSNAQOEISAAFKTL 60
 DB 1 MAQVLRGTVDPPGFDERADAEITLRKAMKGLGTDSEITLTLTSRSNAQOEISAAFKTL 60
 QY 61 FGRDLDDLKSELGKFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 DB 61 FGRDLDDLKSELGKFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAQLF 180
 DB 121 ELRAIKQYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQAQLF 180
 QY 181 QAGELKMGTDDEKFTITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLQQLLAV 240
 DB 181 QAGELKMGTDDEKFTITFGTSVSHLRKVPDKYMTISGFOIEETIDRETSGNLQQLLAV 240
 QY 241 VKSIRSIPAYLAETIIVYAMKAGTDDHTLIRVMSRSEIDLFINIKERKKNPATISYSMI 300
 DB 241 VKSIRSIPAYLAETIIVYAMKAGTDDHTLIRVMSRSEIDLFINIKERKKNPATISYSMI 300
 QY 301 KGDTSGDYKKAALLLCGEDD 320
 DB 301 KGDTSGDYKKAALLLCGEDD 320

RESULT 10
 AAR26276
 ID AAR26276 standard; protein; 319 AA.

XX AC AAR26276;
 XX DT 10-MAR-2003 (revised)
 XX DT 04-FEB-1993 (first entry)
 XX DE CPB-I.
 XX CPB-I; stabilisation; frozen; molten; processed; activity.
 XX OS Homo sapiens.
 XX PN JP04198195-A.
 XX PD 17-JUL-1992.
 XX PF 28-NOV-1990; 90JP-00328286.
 XX PR 28-NOV-1990; 90JP-00328286.
 XX PA (KOMA) KOMA CO LTD.
 XX PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
 XX DR WPI; 1992-288937/35.
 XX PT Stabilisation of CPB-I for drug compen. - by adding basic aminoacid
 XX PT selected from lysine, arginine and/or ornithine.
 XX PS Disclosure; Page 2; 4pp; Japanese.
 XX CC The sequence given is the amino acid sequence of CPB-I. CPB-I was used
 CC within a method which involved adding basic amino acids to it which
 CC resulted in its stabilisation. This lead to the production of CPB-I which
 CC keeps its activity when it is frozen, molten or has been processed by
 CC several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
 XX SQ Sequence 319 AA.

Query Match 99.7%; Score 1595; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AQLRGTVTDVDFPGFDERADAETLRKAMKGLGTEDESILTLTSSRNAOROEISAAPKTLF 61
 DB 1 AQLRGTVTDVDFPGFDERADAETLRKAMKGLGTEDESILTLTSSRNAOROEISAAPKTLF 60
 QY 62 GRDLDDLSKSELTKGFEKLI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 121
 DB 61 GRDLDDLSKSELTKGFEKLI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 122 LRAIKOVYEEYSSLEDDVVDGTSYQRMVLLQANRDPDAGIDEAQVEDQAALFQ 181
 DB 121 LRAIKOVYEEYSSLEDDVVDGTSYQRMVLLQANRDPDAGIDEAQVEDQAALFQ 180
 QY 182 AGEKMGTEDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDETSNGNEQLLAVV 241
 DB 181 AGEKMGTEDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDETSNGNEQLLAVV 240
 QY 242 KSIRSIPIAYLAETLYYAMKAGTDDHTLLRWVMSRSEIDLFINRKEFRKNPATSLYSMTK 301
 DB 241 KSIRSIPIAYLAETLYYAMKAGTDDHTLLRWVMSRSEIDLFINRKEFRKNPATSLYSMTK 300
 QY 302 GDTSGDYKALLLCGEED 320
 DB 301 GDTSGDYKALLLCGEED 319

RESULT 11
 AAR41021
 ID AAR41021 standard; protein; 319 AA.
 XX AC AAR41021;
 XX

DT 29-MAR-1994 (first entry)
 XX DE Calphobindin I (CPB-I).
 XX DE Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
 XX OS Homo sapiens.
 XX PN JP05213769-A.
 XX PD 24-AUG-1993.
 XX PF 04-FEB-1992; 92JP-00019032.
 XX PR 04-FEB-1992; 92JP-00019032.
 XX PA (KOMA) KOMA CO LTD.
 XX PA (KAGA) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.
 XX DR WPI; 1993-299558/38.
 XX PT Protein kinase C inhibitor effective against malignant tumours - con
 XX PT (opt. recombinant) calphobindin I.
 XX PS Claim 1; Page 2-3; 6pp; Japanese.
 XX CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhib
 CC protein kinase C (PKC) and is useful in the treatment of malignant
 CC tumours caused by abnormal activation of PKC. CPB-I is extracted from
 CC human or animal organs and may be applied intravenously, orally,
 CC intramuscularly, percutaneously or rectally
 XX SQ Sequence 319 AA.

Query Match 99.7%; Score 1595; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AQLRGTVTDVDFPGFDERADAETLRKAMKGLGTEDESILTLTSSRNAOROEISAAPKTLF 61
 DB 1 AQLRGTVTDVDFPGFDERADAETLRKAMKGLGTEDESILTLTSSRNAOROEISAAPKTLF 60
 QY 62 GRDLDDLSKSELTKGFEKLI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 121
 DB 61 GRDLDDLSKSELTKGFEKLI VALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTPEE 120
 QY 122 LRAIKOVYEEYSSLEDDVVDGTSYQRMVLLQANRDPDAGIDEAQVEDQAALFQ 181
 DB 121 LRAIKOVYEEYSSLEDDVVDGTSYQRMVLLQANRDPDAGIDEAQVEDQAALFQ 180
 QY 182 AGEKMGTEDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDETSNGNEQLLAVV 241
 DB 181 AGEKMGTEDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETIDETSNGNEQLLAVV 240
 QY 242 KSIRSIPIAYLAETLYYAMKAGTDDHTLLRWVMSRSEIDLFINRKEFRKNPATSLYSMTK 301
 DB 241 KSIRSIPIAYLAETLYYAMKAGTDDHTLLRWVMSRSEIDLFINRKEFRKNPATSLYSMTK 300
 QY 302 GDTSGDYKALLLCGEED 320
 DB 301 GDTSGDYKALLLCGEED 319

RESULT 12
 ABG32550
 ID ABG32550 standard; protein; 319 AA.
 XX AC ABG32550;
 XX DT 29-NOV-2002 (first entry)
 XX DE Human CPB-1 protein.
 XX

KW Human; CPB-I; eye drop; ophthalmological; anaxin V; corneal disease;
 KW calcium/phospholipid binding protein; polyhydric alcohol.
 OS Homo sapiens.
 PN WO200267977-A1.
 XX
 XX
 XX 06-SEP-2002.
 XX
 XX 21-FEB-2002; 2002WO-0P001563.
 XX
 XX 26-FEB-2001; 2001JP-00050297.
 XX
 XX (KOMA) KOMA CO LTD.
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
 XX Naruse H, Sano M, Shinoda Y, Inagi T;
 PI WPI; 2002-674988/72.
 DR
 XX Eye drops for treating e.g. corneal diseases, contain CPB-I and
 PT polyhydric alcohol with specific carbonyl value, without unpleasant
 PT irritation upon dropping but with satisfactory long-term storability.
 XX
 XX Disclosure; Page 13-14; 16pp; Japanese.
 XX
 XX The invention relates to eye drops contain CPB-I (anaxin V) and a
 CC polyhydric alcohol having a carbonyl value of not more than 5wt%
 CC Mol./g. The eyes drops are for treating e.g. corneal diseases. Such eye
 CC drops are without unpleasant irritation upon dropping but with
 CC satisfactory long-term storage stability. The present sequence is the
 CC human CPB-I (calcium/phospholipid binding) protein
 XX
 SQ Sequence 319 AA;
 . Query Match 99.7%; Score 1595; DB 5; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134; Indels 0; Gaps 0;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AOVIRGVTYDPGPERADAEITLRKAMKGLGDESSITLTLTSRNSAOROEISAAFKTLF 61
 Db 1 AOVIRGVTYDPGPERADAEITLRKAMKGLGDESSITLTLTSRNSAOROEISAAFKTLF 60
 QY 62 GRDLDDDKSELTGFEKLIYALMKPSRLYDAVEIKHALKGATNEKVLTEIIASRTPEE 121
 Db 61 GRDLDDDKSELTGFEKLIYALMKPSRLYDAVEIKHALKGATNEKVLTEIIASRTPEE 120
 QY 122 LRAIKQVEEYEGSSLEDDVVDGTSYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 181
 Db 121 LRAIKQVEEYEGSSLEDDVVDGTSYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 180
 QY 182 AGELKMGTDDEKFTITFGTRSVSLRKVPDKYMTISGFOIETITRETSNGN130LLAVV 241
 Db 181 AGELKMGTDDEKFTITFGTRSVSLRKVPDKYMTISGFOIETITRETSNGN130LLAVV 240
 QY 242 KSIRSIPIAYLAFTLYAMKAGAGTDHTLIRWVSSSEIDLFNIRKFRFNPAISLSYMTK 301
 Db 241 KSIRSIPIAYLAFTLYAMKAGAGTDHTLIRWVSSSEIDLFNIRKFRFNPAISLSYMTK 300
 QY 302 GDTSGDYKAKALLLCCEDD 320
 Db 301 GDTSGDYKAKALLLCCEDD 319
 RESULT 13
 ADE55088
 ID ADE55088 standard; protein; 319 AA.
 XX
 XX ADE55088;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE Human Protein P08758, SEQ ID NO 893.

XX
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNJ; Chung.
 OS Homo sapiens.
 PN WO2003016475-A2.
 XX
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GENO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 PA
 PA Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; P08758.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX Claim 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNJ), chronic constriction
 CC injury (CCI) and spared nerve injury (SNJ)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 319 AA;
 . Query Match 99.7%; Score 1595; DB 7; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134; Indels 0; Gaps 0;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AOVIRGVTYDPGPERADAEITLRKAMKGLGDESSITLTLTSRNSAOROEISAAFKTLF 61
 Db 1 AOVIRGVTYDPGPERADAEITLRKAMKGLGDESSITLTLTSRNSAOROEISAAFKTLF 60
 QY 62 GRDLDDDKSELTGFEKLIYALMKPSRLYDAVEIKHALKGATNEKVLTEIIASRTPEE 121
 Db 61 GRDLDDDKSELTGFEKLIYALMKPSRLYDAVEIKHALKGATNEKVLTEIIASRTPEE 120
 QY 122 LRAIKQVEEYEGSSLEDDVVDGTSYYQRMVLVLLQANRPDAGIDEAQVEQDAQALFQ 181

Db 121 LRAIKQVYEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQALFQ 180
 QY 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITRETSNGNEOLLAV 241
 Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITRETSNGNEOLLAV 240
 QY 242 KSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK 301
 Db 241 KSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMTK 300
 QY 302 GDTSGDYKKALLLLCGEED 320
 Db 301 GDTSGDYKKALLLLCGEED 319

RESULT 14

AD56187
 ID AD56187 standard; protein; 319 AA.
 AC AD56187;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P08758, SEQ ID NO 2036.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN W0203016475-A2.
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P08758.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound
 CC modulates its activity is useful for preparing a medicament for treat
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table
 CC the specification) which is differentially expressed during pain. No
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIP
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 319 AA;

Query Match 99.7%; Score 1595; DB 7; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.7e-134;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 2 AOVLRGVTDPGPFDERADAEELRKAMKGLTDEESITLTLSRSMQROEISAFKTL
 Db 1 AOVLRGVTDPGPFDERADAEELRKAMKGLTDEESITLTLSRSMQROEISAFKTL
 QY 62 GRDLDDDKSELNGKFEKLIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIISRPE
 Db 61 GRDLDDDKSELNGKFEKLIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIISRPE
 QY 122 LRAIKQVYEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQALF
 Db 121 LRAIKQVYEEYEGSSLEDDVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEDQALF
 QY 182 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITRETSNGNEOLLAV
 Db 181 AGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFOIETITRETSNGNEOLLAV
 QY 242 KSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMT
 Db 241 KSIRSIPIAYLAETLYYAMKAGCTDDHTLIRVWVSRSSEIDLFNIRKEFRKNFATSLYSMT
 QY 302 GDTSGDYKKALLLLCGEED 320
 Db 301 GDTSGDYKKALLLLCGEED 319

RESULT 15

AAP80242
 ID AAP80242 standard; protein; 320 AA.
 AC AAP80242;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-SEP-1990 (first entry)
 XX
 DE Sequence vascular anticoagulating protein (VAP) VAC-alpha (Asp22).
 XX
 KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activ
 KW antiinflammatory; phospholipase inhibitory.
 XX
 OS Homo sapiens.
 OS
 PN W08807576-A.
 XX
 PD 06-OCT-1988.
 PD
 PF 26-MAR-1988; 88MO-EP000266.
 XX
 PR 28-MAR-1987; 87DE-03710309.
 PR 28-MAR-1987; 87DE-03710364.
 PR 28-MAR-1987; 87DE-03710430.
 PR 04-NOV-1987; 87DE-03737367.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Hauptmann R, Maurerfoggy I, Bodo G, Swetly P, Stracowa C;
 PI Falkner E, Adole G, Reutlingsp CMP;
 XX

DR WPI, 1988-292861/41.
DR N-PSDB; AAN80872.

PT New vascular anti-coagulating proteins - useful as thrombin inhibitors,
PT antiinflammatory agents, etc.

PS Claim 41; Page 171-72; 183pp; German.

CC The DNA is produced by determining the amino acid sequence of isolated
CC and highly purified VAPs, constructing DNA probes on the basis of this
CC sequence, using the probes to search through suitable cDNA libraries,
CC isolating cDNA that hybridises with the probes, by inserting the cDNA
CC into a suitable vector, and using the vector to transform a host
CC organism. VAC-alpha has anticoagulant activity under certain conditions,
CC but loses this activity in the event of severe bleeding. It acts by
CC inhibiting conversion of factor X to factor Xa and conversion of
CC prothrombin to thrombin. It is structurally related to lipocortin I
CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
CC has similar antiinflammatory and phospholipase inhibitory activity.
CC (updated on 25-MAR-2003 to correct PR field.) (updated on 25-MAR-2003 to
CC correct PA field.)

CC Sequence 320 AA;

QY Query Match 99.6%; Score 1594; DB 1; Length 320;

Best Local Similarity 99.4%; Pred. No. 4.6e-134;
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 MAQVLRGVTDPPGDERADAEELRKAMKGLGTEDESILTLTSSRNAQROEISAAEFTL 60
1 MAQVLRGVTDPPGDERADAEELRKAMKGLGTEDESILTLTSSRNAQROEISAAEFTL 60
QY 61 FGRLDLDDKSELTKGFEKLIYALMKPSRLYDAVELKALGAGTNEKVLTEITASRPE 120
61 FGRLDLDDKSELTKGFEKLIYALMKPSRLYDAVELKALGAGTNEKVLTEITASRPE 120
DB 121 ELRAIKQYEEYEGSSLEDVVGDTSSGYQRMVVLQANDPDGIDEAQQVDAQALF 180
121 ELRAIKQYEEYEGSSLEDVVGDTSSGYQRMVVLQANDPDGIDEAQQVDAQALF 180
QY 181 QAGELKMGTDDEKFTTIGTSVSHLRKVPDKWMTISGFOJETIDRETSGLLEQLLAV 240
181 QAGELKMGTDDEKFTTIGTSVSHLRKVPDKWMTISGFOJETIDRETSGLLEQLLAV 240
DB 241 VKSIRSIYAVLAETLYAMKAGTDDHTLIRVMSRSEIDLFNIRKPKFATSLYSMT 300
241 VKSIRSIYAVLAETLYAMKAGTDDHTLIRVMSRSEIDLFNIRKPKFATSLYSMT 300
QY 301 KGDTSQDYKALLLGGEDD 320
301 KGDTSQDYKALLLGGEDD 320
DB 301 KGDTSQDYKALLLGGEDD 320

RESULT 16

AAP80714
ID AAP80714 standard; protein; 320 AA.

XX AAP80714;

DT 25-MAR-2003 (revised)
DT 12-SEP-1990 (first entry)

XX Sequence vascular anticoagulating protein (VAP) VAC-alpha (Glu22).

XX Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant activity;
XX antiinflammatory; phospholipase inhibitory.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 7..18
FT Peptide /label= tryptic peptide P18
FT Peptide 30..45

CC The DNA is produced by determining the amino acid sequence of isolated
CC and highly purified VAPs, constructing DNA probes on the basis of this
CC sequence, using the probes to search through suitable cDNA libraries,
CC isolating cDNA that hybridises with the probes, by inserting the cDNA
CC into a suitable vector, and using the vector to transform a host
CC organism. The posn. of the AA sequences used to construct the probes are
CC given in FT. VAC-alpha has anticoagulant activity under certain
CC conditions, but loses this activity in the event of severe bleeding. It
CC acts by inhibiting conversion of factor X to factor Xa and conversion of
CC prothrombin to thrombin. It is structurally related to lipocortin I
CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
CC has similar antiinflammatory and phospholipase inhibitory activity.
CC (updated on 25-MAR-2003 to correct PR field.) (updated on 25-MAR-2003 to

FT Peptide /label= tryptic peptide P29/I
FT Peptide 51..58
FT Peptide /label= tryptic peptide P14
FT Peptide 59..63
FT Peptide /label= tryptic peptide P15
FT Peptide 64..79
FT Peptide /label= tryptic peptide P27
FT Peptide 80..86
FT Peptide /label= tryptic peptide P20/I
FT Peptide 86..113
FT Peptide /label= BrCN-peptide BrCN15
FT Peptide 90..97
FT Peptide /label= tryptic peptide P16/I
FT Peptide 98..101
FT Peptide /label= tryptic peptide P5
FT Peptide 109..117
FT Peptide /label= tryptic peptide P17
FT Peptide 118..123
FT Peptide /label= tryptic peptide P11/II
FT Peptide 127..151
FT Peptide /label= tryptic peptide P20/I
FT Peptide 187..193
FT Peptide /label= tryptic peptide P11/I
FT Peptide 194..201
FT Peptide /label= tryptic peptide P23/I
FT Peptide 260..271
FT Peptide /label= BrCN-peptide BrCN1
FT Peptide 261..271
FT Peptide /label= tryptic peptide P12
FT Peptide 277..286
FT Peptide /label= tryptic peptide P21
FT Peptide 292..300
FT Peptide /label= tryptic peptide P24
FT Peptide 300..311
FT Peptide /label= BrCN-peptide BrCN4

WO8807576-A.

06-OCT-1988.

26-MAR-1988;

88WO-EP000266.

28-MAR-1987;

87DE-03710309.

28-MAR-1987;

87DE-03710364.

04-NOV-1987;

87DE-03737367.

(BOEH) BOEHRINGER INGELHEIM INT GMBH.

Hauptmann R, Maurerfogel I, Bodo G, Swetly P, Stratawa C;
Falkner E, Adole G, Reutlingsp CMP;

WPI, 1988-292861/41.

N-PSDB; AAN80801.

PT New vascular anti-coagulating proteins - useful as thrombin inhibitors,
PT antiinflammatory agents, etc.

PS Claim 41; Page 171 and Fig 4/1-4/2 and Fig 5/1-5/2; 183pp; German.

CC The DNA is produced by determining the amino acid sequence of isolated
CC and highly purified VAPs, constructing DNA probes on the basis of this
CC sequence, using the probes to search through suitable cDNA libraries,
CC isolating cDNA that hybridises with the probes, by inserting the cDNA
CC into a suitable vector, and using the vector to transform a host
CC organism. The posn. of the AA sequences used to construct the probes are
CC given in FT. VAC-alpha has anticoagulant activity under certain
CC conditions, but loses this activity in the event of severe bleeding. It
CC acts by inhibiting conversion of factor X to factor Xa and conversion of
CC prothrombin to thrombin. It is structurally related to lipocortin I
CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
CC has similar antiinflammatory and phospholipase inhibitory activity.
CC (updated on 25-MAR-2003 to correct PR field.) (updated on 25-MAR-2003 to

CC correct PA field.)

SQ Sequence 320 AA;

Query Match 99.6%; Score 1594; DB 1; Length 320;
 Best Local Similarity 99.4%; Pred. No. 4.6e-134;
 Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVLRGVTDPPGFDERADAEETLRKAMKGLGTEDESIITLTLSRNSAQRQETISAFTL 60
 DB 1 MAQVLRGVTDPPGFDERADAEETLRKAMKGLGTEDESIITLTLSRNSAQRQETISAFTL 60
 QY 61 FGRDLDDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 DB 61 FGRDLDDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 QY 121 ELRAIKQVVEEYSSLEDDVGDTSGYQRMVLVLAQNRDPDAGIDEAQVEDQAQLF 180
 DB 121 ELRAIKQVVEEYSSLEDDVGDTSGYQRMVLVLAQNRDPDAGIDEAQVEDQAQLF 180
 QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
 DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
 QY 241 VKSIRSIPIVLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNFATSLYSMT 300
 DB 241 VKSIRSIPIVLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNFATSLYSMT 300
 QY 301 KGDTSGDYKALLLLCGEDD 320
 DB 301 KGDTSGDYKALLLLCGEDD 320

RESULT 17

AAR11910
 ID AAR11910 standard; protein; 320 AA.

AC AAR11910;
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 25-JUL-1991 (first entry)
 XX Vascular anticoagulant protein.
 DE Vascular anticoagulant protein.
 KW Annexin; anticoagulant; tumour metastasis; fibrin; cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 22..22
 FT /label= Glu, Asp
 PN DE3937607-A.
 PD 16-MAY-1991.
 PF 11-NOV-1989; 89DE-03937607.
 PR 11-NOV-1989; 89DE-03937607.
 PA (BOEH) BOEHRINGER INGELHEIM.
 PI Reuteijings CP;
 DR WPI; 1991-149572/21.

PT Anticoagulants contg. annexin or its analogues and derivs. - used to
 PT treat tumours and to reduce metastases.
 PS Claim 3; Page 11; 17pp; German.

CC This vascular anticoagulant protein (VAC) comprises an annexin. It is

CC formulated with auxiliaries, carriers and/or stabilisers for prevent
 CC tumour cell metastasis. Admin. is by injection, in a pref. dosage of
 CC -0.05 mg/Kg, or using a topical formulation in a dosage of 0.25-10 m
 CC ml soln. or 10g gel. (Updated on 10-MAR-2003 to add missing OS field
 CC (updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 320 AA;

Query Match 99.6%; Score 1594; DB 2; Length 320;
 Best Local Similarity 99.7%; Pred. No. 4.6e-134;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQVLRGVTDPPGFDERADAEETLRKAMKGLGTEDESIITLTLSRNSAQRQETISAFT 60
 DB 1 MAQVLRGVTDPPGFDERADAEETLRKAMKGLGTEDESIITLTLSRNSAQRQETISAFT 60
 QY 61 FGRDLDDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 DB 61 FGRDLDDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 QY 121 ELRAIKQVVEEYSSLEDDVGDTSGYQRMVLVLAQNRDPDAGIDEAQVEDQAQLF 180
 DB 121 ELRAIKQVVEEYSSLEDDVGDTSGYQRMVLVLAQNRDPDAGIDEAQVEDQAQLF 180
 QY 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
 DB 181 QAGELKMGTDDEKFTITFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
 QY 241 VKSIRSIPIVLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNFATSLYSMT 300
 DB 241 VKSIRSIPIVLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNFATSLYSMT 300
 QY 301 KGDTSGDYKALLLLCGEDD 320
 DB 301 KGDTSGDYKALLLLCGEDD 320

RESULT 18

AAR26180
 ID AAR26180 standard; protein; 319 AA.

AC AAR26180;
 DT 10-MAR-2003 (revised)
 DT 04-FEB-1993 (first entry)
 XX CPB-1.
 DE CPB-1.
 KW CPB-1; saccharides; stabilisation; antihemagglutination; dermal disea
 KW corneal disease.
 OS Homo sapiens.
 PN JP04198196-A.
 PD 17-JUL-1992.
 PF 28-NOV-1990; 90JP-00328287.
 PR 28-NOV-1990; 90JP-00328287.
 PA (KOMA) KOMA CO LTD.
 PA (KAGA) KAGAKU OYOBI KESSSEI RYOH.
 DR WPI; 1992-288938/35.

PT Stabilisation of CPB-1 for drug compsn. - contains saccharide selected
 PT from glucose, glucosamine, xylose, saccharose and/or dextran.
 PS Disclosure; Page 2; 4pp; Japanese.

CC The sequence given is the amino acid sequence of CPB-1. CPB-1 was used
 CC within the method of the invention which involved adding saccharides t

it which resulted in its stabilisation. The saccharide was pref. glucose, glucosamine, xylose, saccharose, or dextran. This lead to the production of CPB-I which kept its activity when it had been processed by several treatments. CPB-1 can be used as a medicine for anti-thrombotic, anti-platelet, and corneal diseases. (Updated on 10-MAR-2003 to add missing OS field.)

CC Sequence 319 AA;

Query Match 99.4%; Score 1590; DB 2; Length 319;
Best Local Similarity 99.7%; Pred. No. 1e-133;
Matches 318; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 2 AOVLRGTVDPFGPDERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTLF 61
DB 1 AOVLRGTVDPFGPDERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTLF 60
QY 62 GRDLDDLDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 121
DB 61 GRDLDDLDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
QY 122 LRAIKQVYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
DB 121 LRAIKQVYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 180
QY 182 AGEKMGTEBEKRTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQJLLAV 241
DB 181 AGEKMGTEBEKRTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQJLLAV 240
QY 242 KSIKRSIPAYLAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKPRKNFATSLYSMT 301
DB 241 KSIKRSIPAYLAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKPRKNFATSLYSMT 300
QY 302 GDTSGDYKKALLLLCGEDD 320
DB 301 GDTSGDYKKALLLLCGEDD 319
```

RESULT 19

AAB50864 ID AAB50864 standard; protein; 327 AA.

XX AAB50864;

DT 16-MAR-2001 (first entry)

DE Modified human annexin, SEQ ID NO: 4.

KW Human; annexin; chelation site; nuclear imaging; apoptosis;

KM transplant rejection.

XX Homo sapiens.

OS WO200073332-A1.

PN 07-DEC-2000.

PF 25-MAY-2000; 2000WO-US014324.

PR 01-JUN-1999; 99US-00324096.

XX (UNITW) UNIV WASHINGTON.

PA Tait JF, Brown DS;

DR WPI, 2001-080465/09.

XX N-PSDB; AAC91369.

PT Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue.

PS Claim 15; Page 33-35; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can be effectively chelate a radionuclide and retain yield and with high radiochemical purity. In contrast to conventional products, the modified annexin has a single chelation site remote from the site of biological activity

CC Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.e-133;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MAOVLRGTVDPFGPDERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTL 60
DB 8 MAOVLRGTVDPFGPDERADAEFLRKAMKGLGTDEESILTLTSRNNQROEISAFKTL 67
QY 61 FGRLDDLDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 120
DB 60 FGRLDDLDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTP 127
QY 121 ELRAIKQVYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
DB 120 ELRAIKQVYEEYEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 187
QY 181 AGEKMGTEBEKRTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQJLLAV 240
DB 180 AGEKMGTEBEKRTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRETSNLEQJLLAV 247
QY 241 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKPRKNFATSLYSMT 300
DB 240 VKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVWSRSEIDLFNIRKPRKNFATSLYSMT 307
QY 301 KQDTSGDYKKALLLLCGEDD 320
DB 308 KQDTSGDYKKALLLLCGEDD 327
```

RESULT 20

AAB50865 ID AAB50865 standard; protein; 327 AA.

XX AAB50865;

DT 16-MAR-2001 (first entry)

DE Modified human annexin, SEQ ID NO: 6.

KW Human; annexin; chelation site; nuclear imaging; apoptosis;

KM transplant rejection.

XX Homo sapiens.

OS WO200073332-A1.

PN 07-DEC-2000.

PF 25-MAY-2000; 2000WO-US014324.

PR 01-JUN-1999; 99US-00324096.

XX (UNITW) UNIV WASHINGTON.

PA Tait JF, Brown DS;

DR WPI, 2001-080465/09.

XX N-PSDB; AAC91370.

XX Novel modified annexin useful for imaging vascular thrombi and apoptosis,
 PT has N-terminal chelation site comprising amino acid extension which
 XX comprises a glycine and a cysteine residue.

PS Claim 18; Page 37-38; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chelation
 CC site, which comprises an amino acid extension including a glycine and a
 CC cysteine residue. The modified annexin is useful for imaging vascular
 CC thrombi or apoptosis which is associated with response to a
 CC chemotherapeutic agent or with rejection as a result of transplantation.
 CC The modified annexin can effectively chelate a radionuclide and retain
 CC annexin bioactivity. It can be readily prepared in high radiochemical
 CC yield and with high radiochemical purity. In contrast to conventional
 CC conjugation chemistries that provide a distribution of conjugation
 CC products, the modified annexin has a single chelation site remote from
 CC the site of biological activity

SQ Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
 Best Local Similarity 99.7%; Pred. No. 1.1e-133;

Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAOVLRTVTDPGFERADAEFLRKAMKGLGTEESILTLTSRSNAQROEISAFAKTL 60
 DB 8 MAOVLRTVTDPGFERADAEFLRKAMKGLGTEESILTLTSRSNAQROEISAFAKTL 67
 QY 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 120
 DB 68 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 127
 QY 121 ELRAIKQVVEEYSGSLDDVDVDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 180
 DB 128 ELRAIKQVVEEYSGSLDDVDVDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 187
 QY 181 QAGELKMGTEDEKFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQOLLAV 240
 DB 188 QAGELKMGTEDEKFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQOLLAV 247
 QY 241 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSRSSEIDLFINRKEFRKNPATSLYSMI 300
 DB 248 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSRSSEIDLFINRKEFRKNPATSLYSMI 307
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 308 KGDTSGDYKKALLLLCGEDD 327

RESULT 21

AA850863 ID AA850863 standard; protein; 327 AA.

AC AA850863;

DT 16-MAR-2001 (first entry)

DE Modified human annexin, SEQ ID NO: 2.

KM Human; annexin; chelation site; nuclear imaging; apoptosis;
 KW transplant rejection.

OS Homo sapiens.

PN MO200073332-A1.

PD 07-DEC-2000.

PF 25-MAY-2000; 2000MO-US014324.

PR 01-JUN-1999; 99US-00324096.

XX

PA (UNIT) UNIV WASHINGTON.

XX Tait JF, Brown DS;

XX WPI; 2001-080465/09.

DR N-PsDB; AAC91368.

PT Novel modified annexin useful for imaging vascular thrombi and apopto
 PT has N-terminal chelation site comprising amino acid extension which
 PT comprises a glycine and a cysteine residue.

PS Claim 12; Page 30-31; 39pp; English.

XX The present sequence is a modified annexin having an N-terminal chel
 CC site, which comprises an amino acid extension including a glycine an
 CC cysteine residue. The modified annexin is useful for imaging vascula
 CC thrombi or apoptosis which is associated with response to a
 CC chemotherapeutic agent or with rejection as a result of transplanat
 CC The modified annexin can effectively chelate a radionuclide and reta
 CC annexin bioactivity. It can be readily prepared in high radiochemica
 CC yield and with high radiochemical purity. In contrast to conventiona
 CC conjugation chemistries that provide a distribution of conjugation
 CC products, the modified annexin has a single chelation site remote fr
 CC the site of biological activity

SQ Sequence 327 AA;

Query Match 99.4%; Score 1590; DB 4; Length 327;
 Best Local Similarity 99.7%; Pred. No. 1.1e-133;

Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1 MAOVLRTVTDPGFERADAEFLRKAMKGLGTEESILTLTSRSNAQROEISAFAKTL 120
 DB 8 MAOVLRTVTDPGFERADAEFLRKAMKGLGTEESILTLTSRSNAQROEISAFAKTL 127
 QY 61 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 240
 DB 68 FGRDLDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIIASRTP 247
 QY 121 ELRAIKQVVEEYSGSLDDVDVDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 300
 DB 128 ELRAIKQVVEEYSGSLDDVDVDTSGYQRMVLLQANRPDAGIDEAQVEQDAQALF 307
 QY 181 QAGELKMGTEDEKFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQOLLAV 360
 DB 188 QAGELKMGTEDEKFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQOLLAV 367
 QY 241 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSRSSEIDLFINRKEFRKNPATSLYSMI 420
 DB 248 VKSIRSIPIAYLAETLIYAMKAGTDDHTLIRVWVSRSSEIDLFINRKEFRKNPATSLYSMI 427
 QY 301 KGDTSGDYKKALLLLCGEDD 320
 DB 308 KGDTSGDYKKALLLLCGEDD 327

RESULT 22

AA91363 ID AAP91363 standard; protein; 320 AA.

AC AAP91363;

DT 22-DEC-1989 (first entry)

DE Human lipocortin-V.

KM Human lipocortin-V; lambdaHLipo V-1; anti-inflammatory agent.

OS Homo sapiens.

PN EP30396-A.

PD 30-AUG-1989.

XX

XX 20-FEB-1989; 89EP-00301603.
 PF
 XX
 PR 26-FEB-1988; 88US-00160866.
 XX
 PA (BIOI) BIOGEN INC.
 PA (BIOI) BIOGEN INC.
 XX
 PI Wallner BP, Pepinsky RB, Browning JL;
 WPI; 1989-250486/35.
 DR
 XX Human lipocortin cpds. III, IV, V, and VI - used in treatment of
 PT arthritic, allergic, dermatologic, ophthalmic and collagen disorders
 PT involving inflammatory processes.
 PT
 XX Claim 16; Fig 4; 32pp; English.
 PS
 CC Human lipocortin-V was isolated from a lambda gt10 human peripheral blood
 CC lymphocyte cDNA library with rat lipocortin-V cDNA of lambda Riipo V-1 as
 CC probe. Lipocortins are anti-inflammatory agents and can be used to treat
 CC arthritic, allergic, dermatologic, ophthalmic, and collagen diseases. See
 CC also AAN90598, AAN90599, and AAP91362
 CC
 XX Sequence 320 AA;

Query Match 99.2%; Score 1587; DB 1; Length 320;
 Best Local Similarity 99.4%; Pred. No. 1.9e-133;
 Matches 318; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGVLRGVTDPFGFERADAEFLRKAMKGLTDEESITLTSRSNAQROEISAFAKTL 60
 DB 1 MGVLRGVTDPFGFERADAEFLRKAMKGLTDEESITLTSRSNAQROEISAFAKTL 60
 QY 61 FGRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPE 120
 DB 61 FGRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 121 ELRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 DB 121 ELRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDETSNGNEQLLAV 240
 DB 181 QAGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDETSNGNEQLLAV 240
 QY 241 VKSIRSPAYIAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 DB 241 VKSIRSPAYIAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 QY 301 KGDTSGDYKCALLLLCGEDD 320
 DB 301 KGDTSGDYKCALLLLCGEDD 320

RESULT 23

AAR25718 standard; protein; 319 AA.

XX AAR25718;
 XX AC
 XX 18-JAN-1993 (first entry)
 XX DT
 XX DE
 XX CPB-1.
 XX KM Nerve cell protecting agent; placenta.
 XX OS
 XX Homo sapiens.
 XX JP04173744-A.
 XX PN
 XX 22-JUN-1992.
 XX PD

PF 02-NOV-1990; 90JP-00298036.
 XX
 PR 02-NOV-1990; 90JP-00298036.
 XX
 PA (KOMA) KOMA CO LTD.
 XX
 DR WPI; 1992-255655/31.
 XX
 PT Use of human placenta derived coagulation inhibitor, CPB-1 - for
 PT preventing and treating senile dementia and brain vessel lesions.
 PT
 XX Disclosure; Page 3; 5pp; Japanese.
 PS
 CC The sequence given is a nerve cell protecting agent containing human CPB-
 CC 1. The CPB-1 acts as a growth nutrition factor for nerve cells and the
 CC agent containing it is useful for the prevention and treatment of various
 CC diseases such as senile dementia and brain vessel lesions. The current
 CC agent is derived from human placenta and are free of side effects and
 CC are harmless to the living body
 CC
 XX Sequence 319 AA;

Query Match 97.7%; Score 1563; DB 2; Length 319;
 Best Local Similarity 98.7%; Pred. No. 2.7e-131;
 Matches 315; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AOVLRGVTDPFGFERADAEFLRKAMKGLTDEESITLTSRSNAQROEISAFAKTL 61
 DB 1 AOVLRGVTDPFGFERADAEFLRKAMKGLTDEESITLTSRSNAQROEISAFAKTL 60
 QY 62 GRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPE 121
 DB 61 GRDLDDLSKSELTKGFEKLIYALMKPSRLYDAVEELKALKAGTNEKVLTEIIASRTPE 120
 QY 122 LRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 181
 DB 121 LRAIKQVEEYEGSSLEDVVDGTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALF 180
 QY 182 AGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDETSNGNEQLLAV 241
 DB 181 AGELKMGTDSEKFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDETSNGNEQLLAV 240
 QY 242 KSIRSPAYIAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 301
 DB 241 KSIRSPAYIAETLYYAMKAGTDDHTLIRVMSRSEIDLFNIRKEFRKNFATSLYSMI 300
 QY 302 GDTSGDYKCALLLLCGEDD 320
 DB 301 GDTSGDYKCALLLLCGEDD 319

RESULT 24

AA13924 standard; protein; 319 AA.

XX AA13924;
 XX AC
 XX 13-JUL-1999 (first entry)
 XX DT
 XX DE
 XX S65T GFP variant/hannexin V protein.
 XX OS
 XX GFP; green fluorescent protein; annexin; fusion protein; apoptosis;
 XX fluorescent intensity; anionic phospholipid binding affinity;
 XX asymmetric distribution; plasma membrane phospholipid;
 XX apoptotic cell detection.
 XX KM
 XX Aequorea victoria.
 XX OS
 XX Homo sapiens.
 XX Synthetic.
 XX WO9919470-A2.
 XX PN
 XX 22-APR-1999.
 XX PD

XX 09-OCT-1998; 98WO-US021444.
 PF 09-OCT-1997; 97US-00948276.
 PR (REGC) UNIV CALIFORNIA.
 PA Ernst JD;
 PI WPI; 1999-277634/23.
 DR Bifunctional fusion protein useful for the detection of apoptotic cells.
 XX Claim 2; Page 15-17; 23pp; English.
 PS This sequence represents an example of a protein of the invention. The
 CC proteins are bifunctional Aequorea victoria green fluorescent protein
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide
 CC greater or equal fluorescent intensity and anionic phospholipid binding
 CC affinity, respectively, than do the corresponding unfused GFP and annexin
 CC proteins. An early manifestation of apoptosis is the loss of the
 CC asymmetric distribution of plasma membrane phospholipids, which results
 CC in exposure of anionic phospholipids on the extracellular leaflet of the
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.
 CC The fusion proteins provide for homogeneously labeled annexin, with
 CC fluorescence properties that do not change upon binding membrane
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
 CC membranes
 XX
 SQ Sequence 319 AA;
 Query Match 93.0%; Score 1488.5; DB 2; Length 319;
 Best Local Similarity 94.0%; Pred. No. 1.2e-124;
 Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;
 QY 6 RGVTTDPGPDGRADAEVLRKAMKGLGTDEDSILNLTSSNAQROEIAQEFKTLFGRLD 65
 DB 4 RGVTTDPGPDGRADAEVLRKAMKGLGTDEDSILNLTSSNAQROEIAQEFKTLFGRLD 63
 QY 66 IDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGINEKYLTEIIASRPEELRAI 125
 DB 64 VDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGINEKYLTEIIASRPEELSAI 123
 QY 126 KQYEEBYGSSLEDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQQVEOAQALFOAGEL 185
 DB 124 KQYEEBYGSSLEDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQQVEOAQALFOAGEL 183
 QY 186 KMGTEDEKFTITIGTSSVSHLRKVFDPKWTISGFOIETIDRETSNGLBOLLAAVVSIR 245
 DB 184 KMGTEDEKFTITIGTSSVSHLRKVFDPKWTISGFOIETIDRETSNGLBOLLAAVVSIR 243
 QY 246 SIPAYIAETLYYAMKAGAGTDDHTLIRWVSRSEIDLFINIRKPKKPFATSLYSMIKGDTS 305
 DB 244 SIPAYIAETLYYAMKAGAGTDDHTLIRWVSRSEIDLFINIRKPKKPFATSLYSMIKGDTS 303
 QY 306 GDYKALLLLC-GEED 320
 DB 304 GDYKALLLLC-GEED 319
 RESULT 25
 ID ABB57067 standard; protein; 319 AA.
 AC ABB57067;
 XX 07-MAR-2002 (first entry)
 DT Mouse ischaemic condition related protein sequence SEQ ID NO:136.
 DE Mouse ischaemia; compressive ischaemia; occlusive ischaemia;
 KW

KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX Mus musculus.
 OS WO200189188-A2.
 XX 22-NOV-2001.
 PD 18-MAY-2001; 2001WO-JP004192.
 PF 18-MAY-2000; 2000JP-00145977.
 PR (UNVI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 PI WPI; 2002-034733/04.
 DR N-PSDB; AB199289.
 CC Examining the ischemic condition (e.g. occlusive ischemia) by measur
 CC expression levels of particular genes defined in the specification o
 CC determining the expression profile of a gene group comprising these
 CC genes.
 PS Claim 2; Page 419-421; 2690pp; English.
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of
 CC a gene group in the sample comprising genes selected from (I). The met
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measurin
 CC expression levels of particular genes (AB199289 to AB199912, encodin
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expre
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent
 CC primers for a mouse ischaemic condition related sequence, which are
 CC in the exemplification of the present invention
 XX
 SQ Sequence 319 AA;
 Query Match 93.0%; Score 1488.5; DB 5; Length 319;
 Best Local Similarity 94.0%; Pred. No. 1.2e-124;
 Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps
 QY 6 RGVTTDPGPDGRADAEVLRKAMKGLGTDEDSILNLTSSNAQROEIAQEFKTLFGRLD 65
 DB 4 RGVTTDPGPDGRADAEVLRKAMKGLGTDEDSILNLTSSNAQROEIAQEFKTLFGRLD 63
 QY 66 IDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGINEKYLTEIIASRPEELRAI 125
 DB 64 VDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGINEKYLTEIIASRPEELSAI 123
 QY 126 KQYEEBYGSSLEDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQQVEOAQALFOAGEL 185
 DB 124 KQYEEBYGSSLEDVVGDTSGYYQRMVLVLLQANRPDPAGIDEAQQVEOAQALFOAGEL 183
 QY 186 KMGTEDEKFTITIGTSSVSHLRKVFDPKWTISGFOIETIDRETSNGLBOLLAAVVSIR 245
 DB 184 KMGTEDEKFTITIGTSSVSHLRKVFDPKWTISGFOIETIDRETSNGLBOLLAAVVSIR 243
 QY 246 SIPAYIAETLYYAMKAGAGTDDHTLIRWVSRSEIDLFINIRKPKKPFATSLYSMIKGDTS 305
 DB 244 SIPAYIAETLYYAMKAGAGTDDHTLIRWVSRSEIDLFINIRKPKKPFATSLYSMIKGDTS 303
 QY 306 GDYKALLLLC-GEED 320
 DB 304 GDYKALLLLC-GEED 319
 Search completed: March 25, 2004, 08:04:54

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OM protein - protein search, using sw model

Run on: March 25, 2004, 07:59:40 ; Search time 17 Seconds

(without alignments)
980.144 Million cell updates/sec

Title: US-09-787-923-2

Perfect score: 1600

Sequence: 1 MAQVLRGTVDTPGFERAD.....KDTSGDYKALLLCGEDD 320

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : (SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1595	99.7	319 1	ANX5_HUMAN
2	1545.5	96.6	320 1	ANX5_BOVIN
3	1488.5	93.0	319 1	ANX5_MOUSE
4	1464.5	91.5	318 1	ANX5_RAT
5	1289	80.6	321 1	ANX5_CHICK
6	1096	68.5	323 1	ANX5_CYNPY
7	942	58.9	672 1	ANX6_HUMAN
8	933	58.3	318 1	ANX4_HUMAN
9	931	58.2	318 1	ANX4_PIG
10	931	58.2	672 1	ANX6_RAT
11	927	57.9	672 1	ANX6_HUMAN
12	926	57.9	318 1	ANX4_BOVIN
13	924	57.8	318 1	ANX4_MOUSE
14	911	56.9	318 1	ANX4_CANPA
15	904.5	56.5	671 1	ANX6_CHICK
16	903	56.4	318 1	ANX4_RAT
17	875	54.7	503 1	ANXB_BOVIN
18	873	54.6	503 1	ANXB_RABIT
19	865	54.1	505 1	ANXB_HUMAN
20	857	53.6	503 1	ANXB_MOUSE
21	842.5	52.7	327 1	ANXB_MOUSE
22	832.5	52.0	327 1	ANXB_HUMAN
23	811	50.7	323 1	ANXB_HUMAN
24	809	50.6	323 1	ANXB_MOUSE
25	781	48.8	324 1	ANX3_RAT
26	780	48.8	466 1	ANX7_HUMAN
27	778	48.6	463 1	ANX7_MOUSE
28	771	48.2	618 1	ANXB_BOVIN
29	716	44.8	316 1	ANXC_HYDAT
30	708.5	44.3	338 1	ANXC_HUMAN
31	706	44.1	512 1	ANX2_XENLA
32	704.5	44.0	338 1	ANX2_BOVIN
33	703.5	44.0	338 1	ANX2_RAT

34	701.5	43.8	338 1	ANX2_MOUSE
35	700	43.8	324 1	ANX9_DROME
36	686.5	42.9	320 1	ANXX_DROME
37	685.5	42.8	339 1	ANXB_XENLA
38	679	42.4	315 1	ANXD_HUMAN
39	676.5	42.3	338 1	ANX2_CHICK
40	672.5	42.0	339 1	ANX2_XENLA
41	671	41.9	315 1	ANXD_CANPA
42	659	41.2	346 1	ANX1_RABIT
43	658	41.1	346 1	ANX1_CANVU
44	653	40.8	345 1	ANX1_HORSE
45	653	40.8	345 1	ANX1_HUMAN
46	653	40.8	346 1	ANX1_BOVIN
47	653	40.8	346 1	ANX1_PIG
48	642	40.1	345 1	ANX1_RAT
49	634	39.6	345 1	ANX1_MOUSE
50	633	39.6	343 1	AN12_COLL1
51	598.5	37.4	324 1	ANXA_MOUSE
52	591.5	37.0	324 1	ANXA_HUMAN
53	582.5	36.4	341 1	AN11_COLL1
54	544	34.0	345 1	ANX1_ROSP
55	530	33.1	462 1	ANX9_HUMAN
56	529.5	33.1	462 1	ANX7_DICDI
57	520	32.5	338 1	ANX9_MOUSE
58	449.5	28.1	314 1	ANXA_FRAN
59	206	12.9	337 1	ANX1_CHICK
60	182	11.4	337 1	ANX1_GIALA
61	122.5	7.7	101 1	DVAL_DICVI
62	111.5	7.0	1960 1	MYH9_HUMAN
63	110	6.9	1959 1	MYH9_CHICK
64	108.5	6.8	549 1	THS_PYRO
65	106.5	6.7	550 1	THS_PYRAB
66	104.5	6.5	546 1	THSB_PYRKO
67	104.5	6.5	546 1	THSB_THRKL
68	104.5	6.5	546 1	2294_HUMAN
69	103.5	6.5	545 1	THS_DESSY
70	101.5	6.3	1940 1	MYH3_RAT
71	101	6.3	1557 1	DVAL_DICVI
72	100	6.2	1658 1	YMG7_YEAST
73	100	6.2	2116 1	MYG2_DICDI
74	99.5	6.2	530 1	YG6P_CABEL
75	99.5	6.2	664 1	PARE_STREP
76	99.5	6.2	1035 1	CND3_YEAST
77	99	6.2	1057 1	KEP1_HUMAN
78	98.5	6.2	536 1	MKC7_YEAST
79	98	6.1	399 1	K1CS_BOVIN
80	97.5	6.1	504 1	VPS_AHSV6
81	97	6.1	296 1	G1A2_GIALA
82	97	6.1	464 1	AK15_RAT
83	97	6.1	1163 1	YPT4_CABEL
84	96.5	6.0	437 1	Y532_AQVAE
85	96.5	6.0	437 1	K1CM_MOUSE
86	96.5	6.0	545 1	THSH_THRKH
87	96.5	6.0	857 1	NFM_CHICK
88	96.5	6.0	857 1	HEP1_HELPY
89	96	6.0	618 1	DNAR_DEIRP
90	96	6.0	1690 1	C190_DROME
91	95.5	6.0	300 1	YOGG_BACSU
92	95.5	6.0	720 1	WZC_ECOS7
93	95.5	6.0	720 1	WZC_ECOTI
94	95.5	6.0	841 1	IFP2_PBSBM
95	95.5	6.0	944 1	DNL4_YEAST
96	95	5.9	763 1	CLPL_LACLA
97	95	5.9	1961 1	MYH9_RAT
98	95	5.9	2214 1	POUG_CAZA2
99	94.5	5.9	349 1	ARSA_METVA
100	94.5	5.9	1940 1	MYH3_HUMAN

PO7356	mus mus
P22464	drosoph
P22465	drosoph
P27006	xenopus
P27216	homo sa
P17785	gallus
P24801	xenopus
O29471	canis f
P51662	oryctol
P14087	cavia c
O8hzm6	equus c
P04083	homo sa
P46193	homo sa
P19619	bus scr
P07150	rattus
P10107	mus mus
O92040	columba
O9qz10	mus mus
O9uj72	homo sa
P14950	columba
P24551	rodentia
O76027	homo sa
P24639	dictyos
O9jhg0	mus mus
P51074	fragari
O92108	gallus
O9f657	giardia
P17065	giardia
P35579	homo sa
P14105	gallus
O57762	pyrococ
O9v2g7	pyrococ
O52500	pyrococ
O24730	thermoc
O94822	homo sa
O53546	desulfu
O24702	dictyoc
O03661	sacchar
P08799	dictyos
O06680	sacchar
BE27232	homo sa
P53379	sacchar
P08728	bos tau
O1026	afrikan
P19389	giardia
P24587	rattus r
P41882	caenorh
O66814	aquilex
P08770	mus mus
O24732	thermoc
P16033	gallus
P56105	helicob
P94695	deinococ
O9v185	drosoph
P46318	bacilli
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O08387	sacchar
O06716	lactococ
O62812	rattus r
P36290	c genome
O58542	methano
P11055	homo sa

ALIGNMENTS

ANX5 HUMAN
ID ANX5 HUMAN STANDARD; PRT; 319 AA.
AC P08758;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-1) (Placental anticoagulant protein I) (PAP-1) (PP4)
DE (Thromboplasmin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Annexin C11).
GN ANX5 OR ANX5 OR ENX2 OR PP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88234495; PubMed=2967495;
RA Grundmann U., Abel K.-J., Bohn H., Loebermann H., Lottspeich F.,
RA Kuemper H.;
RT "Characterization of cDNA encoding human placental anticoagulant
RT protein (PP4): homology with the lipocortin family.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3708-3712(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88271329; PubMed=2455636;
RA Maurer-Fogy I., Reutelingersperger C.P.M., Pieters J., Bodo G.,
RA Stratowa C., Hauptmann R.;
RT "Cloning and expression of cDNA for human vascular anticoagulant, a
RT Ca2+-dependent phospholipid-binding protein.";
RL Eur. J. Biochem. 174:585-592(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88273202; PubMed=2968983;
RA Pepinsky R.B., Tizard R., Mateliano R.J., Sinclair L.K., Miller G.T.,
RA Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachter L.,
RA Hession C., Frey A.Z., Wallner B.P.;
RT "Five distinct calcium and phospholipid binding proteins share
RT homology with lipocortin I.";
RL J. Biol. Chem. 263:10799-10811(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88163463; PubMed=2964863;
RA Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;
RT "Primary structure of human placental anticoagulant protein.";
RL Biochemistry 26:8087-8092(1987).
RN [5]
RP SEQUENCE FROM N.A., AND SEQUENCE.
RX MEDLINE=88139278; PubMed=2963810;
RA Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y., Arai K.,
RA Mizoguchi T., Sato F., Yoshizaki H., Hirata M., Miyata T.,
RA Shitara Y., Murata M., Maki M.;
RT "Structure and expression of cDNA for an inhibitor of blood
RT coagulation isolated from human placenta: a new lipocortin-like
RT protein.";
RL J. Biochem. 102:1261-1273(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=88228020; PubMed=2967291;
RA Kaplan R., Jaye M., Burgess W.H., Schlaepfer D.D., Haigler H.T.;
RT "Cloning and expression of cDNA for human endonexin II, a Ca2+ and
RT phospholipid binding protein.";
RL J. Biol. Chem. 263:8037-8043(1988).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung;
MEDLINE=95047484; PubMed=7958998;
RA Fernandez M.P., Morgan R.O., Fernandez M.R., Carcedo M.T.;
RT "The gene encoding human annexin V has a TATA-less promoter with a
RT high G+C content.";
RL Gene 149:253-260(1994).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=94307733; PubMed=8034319;
RA Cookson B.T., Engelhardt S., Smith C., Bamford H.A., Prochazka M.,
RA Tait U.F.;
RT "Organization of the human annexin V (ANX5) gene.";
RL Genomics 20:463-467(1994).
RN [9]
RP SEQUENCE FROM N.A.
RX TISSUE=Muscle, Ovary, and Skin;
MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Bueto K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Mullaly S.J.,
RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP PARTIAL SEQUENCE.
RX MEDLINE=90088443; PubMed=2532007;
RA Rothhut R., Comera C., Cortial S., Haumont P.-Y., Diep Le K.H.,
RA Cavado J.C., Conard J., Russo-Marie F., Lederer F.;
RT "A 32 kDa lipocortin from human mononuclear cells appears to be
RT identical with the placental inhibitor of blood coagulation.";
RL Biochem. J. 263:929-935(1989).
RN [11]
RP SEQUENCE OF 85-130; 258-296 AND 299-319.
RX MEDLINE=87317598; PubMed=2957692;
RA Schlaepfer D.D., Mehlman T., Burgess W.H., Haigler H.T.;
RT "Structural and functional characterization of endonexin II, a
RT calcium and phospholipid-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6078-6082(1987).
RN [12]
RP SEQUENCE OF 84-92.
RX MEDLINE=89066552; PubMed=2974032;
RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=91065314; PubMed=2147412;
RA Huber R., Roemisch J., Paques E.-P.;
RT "The crystal and molecular structure of human annexin V, an
RT anticoagulant protein that binds to calcium and membranes.";
RL EMBO J. 9:3867-3874(1990).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=91085549; PubMed=2148156;
RA Huber R., Schneider M., Mayr I., Roemisch J., Paques E.-P.;
RT "The calcium binding sites in human annexin V by crystal structure
RT analysis at 2.0-A resolution. Implications for membrane binding and
RT calcium channel activity.";
RL FEBS Lett. 275:15-21(1990).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92177413; PubMed=1311770;
RA Huber R., Berendes R., Burger A., Schneider M., Karshikov A.,
RA Luecke H., Roemisch J., Paques E.-P.;

```

RT "Crystal and molecular structure of human annexin V after refinement.
RT Implications for structure, membrane binding and ion channel
RT formation of the annexin family of proteins."
RL J. Mol. Biol. 223:683-704(1992).
RN [16]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=98062349; PubMed=9398511;
RA Kaneko N., Ago H., Matsuda R., Inagaki E., Miyano M.;
RT "Crystal structure of annexin V with its ligand K-201 as a calcium
RT channel activity inhibitor";
RL J. Mol. Biol. 274:16-20(1997).
RN [17]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98118533; PubMed=9435213;
RA Budisa N., Minks C., Medrano F.J., Lutz J., Huber R., Moroder L.;
RT "Residue-specific bioincorporation of non-natural, biologically
RT active amino acids into proteins as possible drug carriers: structure
RT and stability of the per-thioproline mutant of annexin V.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:455-459(1998).
CC -I- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplasmin-specific complex, which
CC is involved in the blood coagulation cascade.
CC -I- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -I- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -I- SIMILARITY: Belongs to the annexin family.
CC -I- SIMILARITY: Contains 4 annexin repeats.
CC -I- CAUTION: This protein has been independently sequenced by at least
CC seven groups under different names!
CC -I- DATABASE: NAME=RED Systems' cytokine source book: Annexin 5;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=185".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12454; CAJ30985.1; -
DR EMBL: M19384; AAB59545.1; -
DR EMBL: M18366; AAA35570.1; -
DR EMBL: M21731; AAA36166.1; -
DR EMBL: D00172; BAA00122.1; -
DR EMBL: J03745; AAA52386.1; -
DR EMBL: U01691; AAB40047.1; -
DR EMBL: U01681; AAB40047.1; JOINED.
DR EMBL: U01682; AAB40047.1; JOINED.
DR EMBL: U01683; AAB40047.1; JOINED.
DR EMBL: U01685; AAB40047.1; JOINED.
DR EMBL: U01686; AAB40047.1; JOINED.
DR EMBL: U01687; AAB40047.1; JOINED.
DR EMBL: U01689; AAB40047.1; JOINED.
DR EMBL: U01690; AAB40047.1; JOINED.
CC -----
Query Match 99.7%; Score 1595; DB 1; Length 319;
Best Local Similarity 100.0%; Pred. No. 1,6e-96;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 AGEIKMGIDEXKFTTIGTSVSHLRKVPDKYMTISGFOIETITRETSNGNLEQILLAVV 241
QY KSISIPAYAEETLYAMKAGTDPHTLIRVWSRSSEIDLFNIRKFRKNFATLSYMT
DB 241 KSISIPAYAEETLYAMKAGTDPHTLIRVWSRSSEIDLFNIRKFRKNFATLSYMT
QY 302 GDTSGDYKALLLCGEDD 320
DB 301 GDTSGDYKALLLCGEDD 319

RESULT 2
ANX5_BOVIN STANDARD; PRT; 320 AA.
ID ANX5_BOVIN
AC P81287;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I
DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
DE (Thromboplasmin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha
DE (Anchotin CII).
GN ANX5 OR ANX5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93041974; PubMed=1420335;
RA Learmonth M.P., Howell S.A., Harris A.C.M., Ames B., Patel Y.,
RA Giannanco I., Bianchi R., Pala G., Ceccarelli P., Donato R.,
RA Green B.N., Altken A.;
RT "Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:
RT structural and phosphorylation differences that suggest distinct
RT biological roles.";
RL Biochim. Biophys. Acta 1160:76-83(1992).
CC -I- FUNCTION: This protein is an anticoagulant protein that acts as
CC an indirect inhibitor of the thromboplasmin-specific complex,
CC which is involved in the blood coagulation cascade.
CC -I- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -I- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -I- SIMILARITY: Belongs to the annexin family.
CC -I- SIMILARITY: Contains 4 annexin repeats.
DR PIR: S27214; S27214.
DR HSSP: P08758; 1ANW.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 4.
DR PRINTS: PD00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
DR Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
KW Acetylation.
FT INTT MET 0 0
FT REPEAT 23 83 ANNEXIN 1.
FT REPEAT 95 155 ANNEXIN 2.
FT REPEAT 179 239 ANNEXIN 3.
FT REPEAT 254 314 ANNEXIN 4.
FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).
FT VARIANT 36 36 S -> T.
FT VARIANT 125 125 K -> E.
SQ SEQUENCE 320 AA; 35942 MW; 50FCB18B5F19CB0 CRC64;

Query Match 96.6%; Score 1545.5; DB 1; Length 320;
Best Local Similarity 96.9%; Pred. No. 2,6e-93;
Matches 310; Conservative 5; Mismatches 4; Indels 1; Gaps 0;

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Db 1 AOVNRTVADPFGFERADAEFLRRAMKGLGDEESILTLTTSRMAQROEIVAFKTLF 60
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Db 61 GRDLIDDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGNTEKLTETIISRPEE 120
Qy 122 LRAIKOYEEEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQ 181
Db 121 LRAIKOYEEEGSSLEDVVGDTSGYQRMVLVLLQANRDPDARIDEAQVEQDAQALFQ 180
Qy 182 AGEIKMGDEKFTTIFGTRSVSHLRKVFDEKMTISGFOIETIDRETSGNLEQULLAVV 241
Db 181 AGEIKMGDEKFTTIFGTRSVSHLRKVFDEKMTISGFOIETIDRETSGNLEQULLAVV 240
Qy 242 KSIRSIPIAYIAETLYAMKAGCTDHTLIRWVSRSEIDLFNIRKFRKNFATISLYSMIK 301
Db 241 KSIRSIPIAYIAETLYAMKAGCTDHTLIRWVSRSEIDLFNIRKFRKNFATISLYSMIK 300
Qy 302 GDTSGDYKALLILLC-GEED 320
Db 301 GDTSGDYKALLILLCGEED 320

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RESULT 3

ANX5 MOUSE

ID _ANX5 MOUSE STANDARD; PRT; 319 AA.

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AC P48036;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
DE (CBP-I) (Placental anticoagulant protein I) (PAP-I) (Pp4)
DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
DE (Anchoxin CII)
DE ANXAS OR ANXS.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal cavity;
RX MEDLINE=96422179; PubMed=824796;
RA Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez M.P.;
RT "Mouse annexin V chromosomal localization, cDNA sequence
RT conservation, and molecular evolution.";
RL Genomics 31:151-157 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Adachi T., Kojima K., Fukuoaka S.-I., Ogawa H., Matsumoto I.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX MEDLINE=99072820; PubMed=9854034;
RA Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
RA Fernandez M.P.;
RT "Mouse annexin V genomic organization includes an endogenous
RT retrovirus.";
RL J. Biochem. 337:125-131 (1999).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade.
CC -1- SUBUNIT: Monomer. Binds ATRX (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
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CC EMBL; U29396; AAC52530.1; -
CC DR EMBL; D63423; BAA09728.1; -
CC DR EMBL; AJ230108; CA13092.1; -
CC DR EMBL; AJ230110; CA13092.1; JOINED.
CC DR EMBL; AJ230111; CA13092.1; JOINED.
CC DR EMBL; AJ230114; CA13092.1; JOINED.
CC DR EMBL; AJ230116; CA13092.1; JOINED.
CC DR EMBL; AJ230118; CA13092.1; JOINED.
CC DR EMBL; AJ230119; CA13092.1; JOINED.
CC DR EMBL; AJ230121; CA13092.1; JOINED.
CC DR EMBL; AJ230122; CA13092.1; JOINED.
CC DR EMBL; AJ230123; CA13092.1; JOINED.
CC DR EMBL; AJ230124; CA13092.1; JOINED.
CC DR HSP; P14668; IAB8.
CC DR SWISS-2DPAGE; P48036; MOUSE.
CC DR MGD; MGI:106008; Anxa5.
CC DR InterPro; IPR001464; Annexin.
CC DR Pfam; PF00191; annexin; 4.
CC DR PRINTS; PR00196; ANNEXIN.
CC DR PRODOM; PD000143; ANNEXIN; 4.
CC DR SMART; SM00335; ANX; 4.
CC DR PROSITE; PS00223; ANNEXIN; 4.
CC KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
CC KW Placenta.
CC FT REPEAT 22 82 ANNEXIN 1.
CC FT REPEAT 94 154 ANNEXIN 2.
CC FT REPEAT 178 238 ANNEXIN 3.
CC FT REPEAT 253 313 ANNEXIN 4.
CC SQ SEQUENCE 319 AA; 35752 MW; 55055BAF2B1C36B7 CRC64;

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Query Match 93.0%; Score 1488.5; DB 1; Length 319;
Best Local Similarity 94.0%; Pred. No. 1.3e-89;
Matches 297; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

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Qy 6 RGVTDLPFGFDEBRADAEFLRRAMKGLGDEESILTLTTSRMAQROEIVAFKTLFGRDL 65
Db 4 RGVTDLPFGFDEBRADAEFLRRAMKGLGDEESILTLTTSRMAQROEIVAFKTLFGRDL 63
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Qy 126 KOYEEEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 185
Db 124 KOYEEEGSSLEDVVGDTSGYQRMVLVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 183
Qy 186 KWGDEEKFTTIFGTRSVSHLRKVFDEKMTISGFOIETIDRETSGNLEQULLAVVKSIR 245
Db 184 KWGDEEKFTTIFGTRSVSHLRKVFDEKMTISGFOIETIDRETSGNLEQULLAVVKSIR 243
Qy 246 SIPAYIAETLYAMKAGCTDHTLIRWVSRSEIDLFNIRKFRKNFATISLYSMIKGTS 305
Db 244 SIPAYIAETLYAMKAGCTDHTLIRWVSRSEIDLFNIRKFRKNFATISLYSMIKGTS 303
Qy 306 GDYKALLILLC-GEED 320
Db 304 GDYKALLILLCGEED 319

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RESULT 4

ANX5 RAT

ID _ANX5 RAT STANDARD; PRT; 318 AA.

```

AC P14668;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)

```

DE (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4)
 DE (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
 DE (Anchoring CII).
 GN ANXAS OR ANXS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68273202; PubMed=2968983;
 RA Pelpinsky R.B., Rizard R., Nattaliano R.U., Sinclair L.K.,
 RA Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
 RA Pratt D., Wächter L., Hession C., Frey A.Z., Wallner B.P.;
 RT "Five distinct calcium and phospholipid binding proteins share
 RT homology with lipocortin I";
 RL J. Biol. Chem. 263:10799-10811(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar;
 RX MEDLINE=96035863; PubMed=7556178;
 RA Imai Y., Kohsaka S.;
 RT "Structure of rat annexin V gene and molecular diversity of its
 RT transcripts";
 RL Eur. J. Biochem. 232:327-334(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=93369587; PubMed=8362244;
 RA Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Rat annexin V crystal structure: Ca(2+)-induced conformational
 RT changes";
 RL Science 261:1321-1324(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC TISSUE=Kidney;
 RX MEDLINE=96069783; PubMed=7583670;
 RA Swaitjo M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.;
 RT "Ca(2+)-bridging mechanism and phospholipid head group recognition in
 RT the membrane-binding protein annexin V";
 RL Nat. Struct. Biol. 2:968-974(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2-319.
 RX MEDLINE=98272673; PubMed=9609693;
 RA Campos B., Mo Y.D., Mealy T.R., Li C.W., Swaitjo M.A., Balch C.,
 RA Head J.F., Reizinger G., Dedman J.R., Seaton B.A.;
 RT "Mutational and crystallographic analyses of interfacial residues in
 RT annexin V suggest direct interactions with phospholipid membrane
 RT components";
 RL Biochemistry 37:8004-8010(1998).
 RN [6]
 RP INTERACTION WITH DNMT1.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=96301899; PubMed=8667030;
 RA Ohnawa K., Imai Y., Ito D., Kohsaka S.;
 RT "Molecular cloning and characterization of annexin V-binding proteins
 RT with highly hydrophilic peptide structure";
 RL J. Neurochem. 67:89-97(1996).
 CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
 CC indirect inhibitor of the thromboplastin-specific complex, which
 CC is involved in the blood coagulation cascade.
 CC -1- SUBUNIT: Monomer. Binds ATRX and DNMT1.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC or send an email to: license@isb-sib.ch).

CC EMBL: M21730; AAA41512.1; -
 DR EMBL: D42137; BAA07708.1; -
 DR EMBL: D42129; BAA07708.1; JOINED
 DR EMBL: D42130; BAA07708.1; JOINED
 DR EMBL: D63337; BAA07708.1; JOINED
 DR EMBL: D42131; BAA07708.1; JOINED
 DR EMBL: D42132; BAA07708.1; JOINED
 DR EMBL: D42133; BAA07708.1; JOINED
 DR EMBL: D42134; BAA07708.1; JOINED
 DR EMBL: D42135; BAA07708.1; JOINED
 DR EMBL: D42136; BAA07708.1; JOINED
 DR PIR: C9250; LURTS.
 DR PDB: 2ZAN; 30-NOV-94.
 DR PDB: 1A8A; 17-JUN-98.
 DR PDB: 1A8B; 17-JUN-98.
 DR PDB: 1BC0; 13-JAN-99.
 DR PDB: 1BC1; 13-JAN-99.
 DR PDB: 1BC3; 13-JAN-99.
 DR PDB: 1BCW; 13-JAN-99.
 DR PDB: 1BCY; 13-JAN-99.
 DR PDB: 1BCZ; 13-JAN-99.
 DR PDB: 1GSN; 13-MAR-02.
 DR PDB: 1N41; 04-FEB-03.
 DR PDB: 1N42; 04-FEB-03.
 DR PDB: 1N44; 04-FEB-03.
 DR InterPro: IPR001464; Annexin.
 DR Pfam: PR00191; annexin; 4.
 DR PRINTS: PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART: SM00335; ANX; 4.
 DR PROSITE: PS00223; ANNEXIN; 4.
 DR Annexin: Calcium/phospholipid-binding; Repeat; Blood coagulation;
 KM Placenta; Acetylation; 3D-structure.
 KW INIT MET 0
 FT REPEAT 20 80 ANNEXIN 1.
 FT REPEAT 92 152 ANNEXIN 2.
 FT REPEAT 176 236 ANNEXIN 3.
 FT REPEAT 251 311 ANNEXIN 4.
 FT MOD RES 1 1 ACETYLATION.
 FT TURN 10 11
 FT HELIX 14 25
 FT HELIX 32 39
 FT TURN 40 41
 FT HELIX 44 58
 FT HELIX 62 69
 FT HELIX 72 82
 FT HELIX 85 97
 FT HELIX 104 113
 FT HELIX 116 130
 FT HELIX 134 141
 FT HELIX 144 154
 FT TURN 155 155
 FT HELIX 166 179
 FT TURN 180 182
 FT HELIX 188 197
 FT HELIX 200 214
 FT HELIX 218 225
 FT HELIX 228 242
 FT HELIX 244 256
 FT HELIX 263 273
 FT TURN 274 277
 FT HELIX 278 289
 FT HELIX 293 300
 FT HELIX 303 313
 SO SEQUENCE 318 AA; 35613 MW; 1A755A7C11FA1ICE CRC64;
 Query March 91.5%; Score 1464.5; DB 1; Length 318;
 Best Local Similarity 92.1%; Pred. No. 4.6e-68;
 Matches 292; Conservative 12; Mismatches 12; Indels 1; Gap

Qy

5 LRGTVDTPGFDEADATLRKMKGLGDEESLITLITRSNANROEISAAFTTLFG

Db 2 LRGTVDPSGFDGRADAEVLNRKAMKGLTDEDSIINLTARSNAQRQIAE3FKTLFGRD 61
 Qy 65 LLDLKSRLTGKFEELIVALKKPSRLYDAVELKHALKAGNMETKLTETIIA3RPEELRA 124
 Db 62 LVNDKSSLTGKFEELIVALKKPSRLYDAVELKHALKAGNDEKLTETIIA3RPEELRA 121
 Qy 125 IKQVEEYEGSSLEDDVVDGTSGYYQRMVLLQANRPDGDIDEAQVEODAOALFOAGE 184
 Db 122 IKQVEEYEGSSLEDDVVDGTSGYYQRMVLLQANRPDGDIDEAQVEODAOALFOAGE 181
 Qy 185 LKMGDEBEKFTITIGTRSVSHLRKVFEDKXMTISGFQIBETIDRETSNLEQILLAVKSI 244
 Db 182 LKMGDEBEKFTITIGTRSVSHLRKVFEDKXMTISGFQIBETIDRETSNLEQILLAVKSI 241
 Qy 245 RSIPIAYIAETLYAMKAGATDHDHILIRVRSSEIDLENIRKFRKXPATSLYSNMGDT 304
 Db 242 RSIPIAYIAETLYAMKAGATDHDHILIRVRSSEIDLENIRKFRKXPATSLYSNMGDT 301
 Qy 305 SGDYKKALLLIC-GEED 320
 Db 302 SGDYKKALLLIC-GEED 318

RESULT 5

ANX5_CHICK STANDARD; PRT; 321 AA.
 ID ANX5_CHICK STANDARD; PRT; 321 AA.
 AC P17153;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-1) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplasmin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchotin CII).
 DE ANX5 OR ANX5.
 GN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=8816917; PubMed=283522;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.,
 RT "The structure of anchotin CII, a collagen binding protein isolated from chondrocyte membrane.";
 RL J. Biol. Chem. 263:5921-5925(1988).
 RN [2]
 RP SUGGEST SEQUENCING ERROR.
 RX MEDLINE=90020458; PubMed=2552626;
 RA Moss S.E., Crumpton M.J.;
 RT "Alternative splicing or cloning artefact?";
 RL Trends Biochem. Sci. 14:325-325(1989).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=90243721; PubMed=2159478;
 RA Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.,
 RT "The structure of anchotin CII, a collagen binding protein isolated from chondrocyte membrane.";
 RL J. Biol. Chem. 265:8344-8344(1990).
 RN [4]
 RP REVISIONS.
 RX Pfaeffle M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O., Yamada Y., Garrone R., von der Mark K.,
 RL EMBO J. 9:1336-1336(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=white leghorn; TISSUE=Liver;
 RX MEDLINE=94215900; PubMed=8163186;
 RA Fernandez M.P., Fernandez M.R., Morgan R.O.;
 RT "Structure of the gene encoding anchotin CII (chick annexin V).";

RL Gene 141:179-186(1994).
 RN [6]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=93249384; PubMed=8484740;
 RA Boustead C.M., Brown R., Walker J.H.;
 RT "Isolation, characterization and localization of annexin V from chicken liver.";
 RL Biochem. J. 291:601-608(1993).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93229489; PubMed=8471604;
 RA Bevilacqua M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.;
 RT "Structure of chicken annexin V at 2.25-A resolution.";
 RL Biochemistry 32:3923-3929(1993).
 CC -1- FUNCTION: Collagen-binding protein.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
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 CC -----
 CC EMBL; M30971; AAA48591.1; ALT_SEQ.
 CC EMBL; U01680; AAB39917.1; -.
 CC EMBL; U01671; AAB39917.1; JOINED.
 CC EMBL; U01672; AAB39917.1; JOINED.
 CC EMBL; U01673; AAB39917.1; JOINED.
 CC EMBL; U01675; AAB39917.1; JOINED.
 CC EMBL; U01676; AAB39917.1; JOINED.
 CC EMBL; U01677; AAB39917.1; JOINED.
 CC EMBL; U01678; AAB39917.1; JOINED.
 CC EMBL; U01679; AAB39917.1; JOINED.
 CC PIR; A35381; LUCH5.
 CC PDB; 1ALA; 31-OCT-93.
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC PRODOM; PD000143; Annexin; 4.
 CC SMART; SM00335; ANX; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
 CC REPEAT 24
 CC REPEAT 96 156
 CC REPEAT 180 240
 CC REPEAT 255 315
 CC CONFLICT 168 168
 CC TURN 13 14
 CC TURN 17 28
 CC TURN 35 44
 CC TURN 47 61
 CC TURN 65 72
 CC TURN 75 85
 CC TURN 88 90
 CC TURN 91 100
 CC TURN 107 116
 CC TURN 119 133
 CC TURN 137 144
 CC TURN 147 157
 CC TURN 158 158
 CC TURN 159 184
 CC TURN 185 187
 CC TURN 191 200
 CC TURN 203 217
 CC TURN 221 224
 CC TURN 232 245
 CC TURN 247 259
 CC TURN 247 259

FT HELIX 266 275
 FT TURN 276 280
 FT HELIX 281 292
 FT HELIX 296 303
 FT HELIX 306 316
 SQ SEQUENCE 321 AA; 36198 MW; 43E2983F86797025 CRC64;

Query Match 80.6%; Score 1289; DB 1; Length 321;
 Best Local Similarity 78.4%; Pred. No. 1.1e-76;
 Matches 251; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

QY 1 MAQVLRGTVDPFGDERADAEATLRKAMKGLGTDEESITLTLSRNSAOROEISAARKTL 60
 DB 1 MAKYRGTVAPSPFADADAELRKAMKMGTEETILKILTSRNNAROEIASAFKTL 60
 QY 61 FGRLDLDLKSSELTGFEKLIYALMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 DB 61 FGRLDLDLKSSELTGFEKLIYALMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
 QY 121 ELRAIKQVVEEYSSLEDVVDGTSYQORMVLVLLQANRPDAGIDEAQQEQAALF 180
 DB 121 EVQNIKQVYMOEYEALEDEKITEGSHFQRLVLLQANRPDQGVDEALYKDAQVLF 180
 QY 181 QAGELKMGTEDEEFTITFGTRSVSHLRKVPDKMTISGFQIETIDRETSNLEQILLAV 240
 DB 181 RAGELKMGTEDEEFTITLTGRSVSHLRKVPDKMTISGFQIETIDRETSNLEQILLAV 240
 QY 241 VKSIRSIPAVLAETLYYAMKAGTDHTLIRVWSRSEIDLFNIRKERNKFNATSLYSMT 300
 DB 241 VKCIRSVPAVFATLYYSMKAGTDHTLIRVWSRSEIDLIRHEFRNFKNSLYOMI 300
 QY 301 KQPTSGDYKALLLCGEDD 320
 DB 301 QKDTSGDYKALLLCGGDD 320

RESULT 6

ANX5_CYNPY STANDARD; PRT; 323 AA.

ID ANX5_CYNPY STANDARD; PRT; 323 AA.
 AC P70075;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A5 (Annexin V).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
 NCBI_Taxid=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Yamamoto T., Hikono T., Abe S.I.;
 RT "Differential expression of annexin V during spermatogenesis in the
 RT newt Cynops pyrrhogaster.";
 RL Dev. Genes Evol. 206:64-71(1996).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
 CC membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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CC EMBL: D64134; BAA11012.1;
 CC DR HSSP: P08758; IAAV.
 CC DR InterPro: IPR001464; Annexin.

DR Pfam: PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom: PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR KW Annexin; Calcium/phospholipid-binding; Repeat.
 FT REPEAT 26 86 ANNEXIN 1.
 FT REPEAT 98 158 ANNEXIN 2.
 FT REPEAT 182 242 ANNEXIN 3.
 FT REPEAT 257 317 ANNEXIN 4.
 SQ SEQUENCE 323 AA; 35981 MW; 044B31AC28164CE2 CRC64;

Query Match 68.5%; Score 1096; DB 1; Length 323;
 Best Local Similarity 68.3%; Pred. No. 3.4e-64;
 Matches 215; Conservative 45; Mismatches 55; Indels 0; Gaps 0;

QY 6 RGTVDTPGDERADAEATLRKAMKGLGTDEESITLTLSRNSAOROEISAARKTL 60
 DB 8 KGTVDAPDPFNKEDAEATLRKAMKGLGTDEETILKILTSRNSKORQIALTYKTLFGRL 60
 QY 66 LDDLSSELTGFEKLIYALMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELR 120
 DB 66 TDDLSSELTGFEKLIYALMPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPELR 120
 QY 126 KQYEEYSSLEDVVDGTSYQORMVLVLLQANRPDAGIDEAQQEQAALF 180
 DB 126 KQYEEYSSLEDVVDGTSYQORMVLVLLQANRPDAGIDEAQQEQAALF 180
 QY 128 KETVKKFSDLEKIDVGTSGNFKELVSLVQANRPDQGVDEALYKDAQVLF 240
 DB 128 KETVKKFSDLEKIDVGTSGNFKELVSLVQANRPDQGVDEALYKDAQVLF 240
 QY 186 KMGTEDEEFTITFGTRSVSHLRKVPDKMTISGFQIETIDRETSNLEQILLAV 300
 DB 186 KMGTEDEEFTITLTGRSVSHLRKVPDKMTISGFQIETIDRETSNLEQILLAV 300
 QY 246 SIPAVLAETLYYAMKAGTDHTLIRVWSRSEIDLFNIRKERNKFNATSLYSMT 300
 DB 246 SIQYLAEVLYYSMKAGTDHTLIRVWSRSEIDLFNIRKERNKFNATSLYSMT 300
 QY 306 GDYKALLLCGEDD 320
 DB 308 GDYKALLLCGEID 322

RESULT 7

ANX6_MOUSE STANDARD; PRT; 672 AA.

ID ANX6_MOUSE STANDARD; PRT; 672 AA.
 AC P14824;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
 DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 GN ANXA6 OR ANX6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/c;
 RX MEDLINE=89030687; PubMed=2972541;
 RA Moss S.E., Crumpton M.R., Crumpton M.J.;
 RT "Molecular cloning of murine p68, a Ca2+-binding protein of the
 RT lipocortin family.";
 RL Eur. J. Biochem. 177:21-27(1988).
 CC -1- FUNCTION: May associate with CD21. May regulate the release of
 CC Ca2+ from intracellular stores.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 8 annexin repeats.
 CC -----
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DR EMBL; X13460; CAA31808.1; -
DR PIR; S01786; S01786.
DR HSSP; P79134; 1AVC.
DR MGI; MGI.88255; Annex6.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SM00335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 8.
DR Annexin; Calcium/phospholipid-binding; Repeat.
KW ANXIN 1.
FT REPEAT 28 88 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
SQ SEQUENCE 672 AA; 75755 MW; 2D85C1DD235FC76 CRC64;

Query Match 58.9%; Score 942; DB 1; Length 672;
Best Local Similarity 59.4%; Pred. No. 7.7e-54;
Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

QY 6 RGTVTDFPGFDERADATTLRKAMKGLTDESEIITLLTSSNROEISAFTLEPRDL 65
DB 10 RGSVHDFPFDANODAEALYTKMGKSGSDKESILELTSSNNKORQICOSTYSLVKDL 69
QY 66 LDDLKSELTKGFEKLIVALKMPSRLYDAVELKHALKGAGTNEKYLTEIIASRPEELRAI 125
DB 70 IEDLKELTKGFEKLIVALKMPSRLYDAVELKHALKGAGTNEKYLTEIIASRPEELRAI 129
QY 126 KQYEEYEGSSLEDDVVGDTSGYQRMVLLQANDPDAGIDAEQVEDQALFQAGEL 185
DB 130 VAAVKAYERDESIDIGDTSGHFKMLVLLQGTRENDVVEDLVQDVLYAGEL 189
QY 186 KNGTDEKETTIGRTSVSHIRKVPKMTISFOIETIDRTSGNLEQLIAVVKSLR 245
DB 190 KNGTDAQPIYILGNSSKQHLRLVPEYKTKTEKPIEASIRGELSGDFEMLAVVKIR 249
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVMSRSRIDLFNIRKERNKPAISLVSMIGDTS 305
DB 250 SIPEYFAERLFRAMKGLGRDNLIRIVWSRSELDMLDIRIETRYEKSLVSMKNDTS 309
QY 306 GDYKALLLLCGEDD 320
DB 310 GEYKALLLTCGGDD 324

RESULT 8
ANX4 HUMAN
ID ANX4 HUMAN STANDARD; PRT; 318 AA.
AC P09525; Q96F33; Q9BWK1;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A4 (Annexin IV) (lipocortin IV) (Endonexin I) (Chromobindin 4) (PpA-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/P41).
DE (P33/P41).
GN ANX4 OR ANX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88309022; PubMed=2970257;
RA Grundmann U., Amani E., Abel K.-J., Kuepper H.A.;
RT "Isolation and expression of cDNA coding for a new member of the
RT phospholipase A2 inhibitor family.";
RL Behring Inst. Mitt. 82:59-67(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92155721; PubMed=1346776;
RA Tait J.F., Smith C., Frankberry D.A., Miao C.H., Adler D.A.,
RA Distchech C.M.;
RT "Chromosomal mapping of the human annexin IV (ANX4) gene.";
RL Genomics 12:313-318(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9729215; PubMed=9084877;
RA Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
RA Matsumoto I.;
RT "Characterization of human p33/41 (annexin IV), a Ca2+ dependent
RT carbohydrate-binding protein with monoclonal anti-annexin IV
RL antibodies, AS11 and AS17.";
RL Biol. Pharm. Bull. 20:224-229(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye, and Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 26-55; 98-123 AND 279-307.
RX MEDLINE=8906652; PubMed=2974032;
RA Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
RA de Haen C.;
RT "Sedimentation equilibrium analysis of five lipocortin-related
RT phospholipase A2 inhibitors from human placenta. Evidence against a
RT mechanistically relevant association between enzyme and inhibitor.";
RL J. Biol. Chem. 263:18657-18663(1988).
RN [6]
RP SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
RX MEDLINE=89118212; PubMed=2975506;
RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T.,
RA Hendrickson L.E., Fujikawa K.;
RT "Placental anticoagulant proteins: isolation and comparative
RT characterization four members of the lipocortin family.";
RL Biochemistry 27:6268-6276(1988).
RN [7]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=91073383; PubMed=2254922;
RA Fremont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.;
RT "Crystalization and preliminary x-ray crystallographic studies of
RT human placental annexin IV.";
RL J. Mol. Biol. 216:219-221(1990).
CC -I- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (By similarity).

DT	01-ANX-1988	(Rel. 08, Created)	
DT	01-ANX-1988	(Rel. 08, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin		
DE	(Protein II) (P32.5) (Placental anticoagulant protein I) (PAF-II)		
DE	(PP4-X) (35-beta calcimedlin).		
GN	ANKX4 OR ANX4		
OS	Sus scrofa (Pig).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RP	[1]		
RC	SEQUENCE.		
RC	TISSUE=Intestinal epithelium;		
RX	MEDLINE=87275850; PubMed=2956093;		
RA	Weber K., Johnson N., Plesmann U., Van P.N., Soling H.-D., Ampe C		
RA	Vanderkrokov J.;		
RT	"The amino acid sequence of protein II and its phosphorylation site		
RT	for protein kinase C; the domain structure Ca2+-modulated lipid		
RT	binding proteins.";		
RL	EMBO J. 6:1599-1604(1987).		
RN	[2]		
RP	SEQUENCE OF 1-126 FROM N.A.		
RC	TISSUE=Small intestine;		
RX	MEDLINE=96327607; PubMed=8672129;		
RA	Winteroe A.K., Frelholm M., Davies W.;		
RA	"Evaluation and characterization of a porcine small intestine cDNA		
RT	library: analysis of 839 clones.";		
RL	Mamm. Genome 7:509-517(1996).		
CC	-1- FUNCTION: Calcium/phospholipid-binding protein which promotes		
CC	membrane fusion and is involved in exocytosis (By similarity).		
CC	-1- SUBUNIT: Monomer.		
CC	-1- DOMAIN: A pair of annexin repeats may form one binding site for		
CC	calcium and phospholipid.		
CC	-1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity		
CC	-1- SIMILARITY: Belongs to the annexin family.		
CC	-1- SIMILARITY: Contains 4 annexin repeats.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/an		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; F14682; CAA23194.1; -		
DR	PIR: A27107; LUPG4.		
DR	HSP; P13214; IANN.		
DR	InterPro; IPR001464; Annexin.		
DR	Pfam; PF00191; annexin.4.		
DR	PRINTS; PR00196; ANNEXIN.		
DR	ProDom; PD000143; Annexin.4.		
DR	SMART; SM00335; ANX.4.		
DR	PROSITE; PS00223; ANNEXIN.4.		
KW	Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;		
KW	Acetylation.		
FT	INIT MET	0	ANNEXIN 1.
FT	REPEAT	22	82 ANNEXIN 2.
FT	REPEAT	94	154 ANNEXIN 3.
FT	REPEAT	178	238 ANNEXIN 4.
FT	REPEAT	253	313 ANNEXIN 4.
FT	MOD RES	1	1 ACETYLTATION (PROBABLE).
FT	MOD RES	6	6 PHOSPHORYLTATION (BY PKC).
SO	SEQUENCE	318 AA; 35697 MW; FA7D9CE3B7C631E8 CR64;	
QY	Query Match	58.2%; Score 931; DB 1; Length 318;	
QY	Best Local Similarity	58.9%; Pred. No. 1.6e-53;	
QY	Matches 185; Conservative	51; Mismatches 78; Indels 0; Gaps	
DB	5 GYTKASGNAEDAQTRKMKGLGTDEDAIIISVLAYSTAQRORIFRAYKSTGR		

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QY 67.DDLKSELTKFEKLIIVALKMPSRLVDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 126
D 65.DDLKSELTKFEKLIIVALKMPSRLVDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 124
QY 127.QVVEEYSSSLDDVDVGTSGYQMLVYLQANRDPDAGIDEAQVEDQAALFQAGELK 186
D 125.QVYQYGRSLIEDIRSDTSFMPQVIVLSAGCRDEBNYDADLVQDADLYEAGBKK 184
QY 187.WGTDEEFTITFGTSVSHLRKVPDKWMTISGFQIEETIDETSQNLQOLLAVYKSI 246
D 185.WGTDEEFTITFGTSVSHLRKVPDKWMTISGFQIEETIDETSQNLQOLLAVYKSI 244
QY 247.IPAYLAETLYYAMKAGTDHTLIRVWVSREIDLPNIRKFRKQNPATSLYSMTKGDTS 306
D 245.KSAFAERLYKSMKGLGTDNTLIRVWVSRAEIMDMIRANFKLYGKSLYSFTKGDTS 304
QY 307.DYKXALLLCGEDD 320
D 305.DYKXALLLCGEDD 318

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RESULT 10

ANK6_RAT STANDARD; PRT: 672 AA.

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AC P48037;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CP3-II)
DE (Calcium-binding protein CATA 65/67).
GN ANX6 OR ANX6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=liver;
RX MEDLINE=9531313; PubMed=7607247;
RA Fan H., Josic D., Lim Y.P., Reutter W.;
RT "cDNA cloning and tissue-specific regulation of expression of rat
RT calcium-binding protein 65/67. Identification as a homologue of
RT annexin VI."
RL Eur. J. Biochem. 230:741-751(1995).
CC - FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores.
CC - DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC - MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC - SIMILARITY: Belongs to the annexin family.
CC - SIMILARITY: Contains 8 annexin repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X86086; CAA6040.1; -
DR PIR; S65683; S52844.
DR HSSP; P79134; IAVC.
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 8.
DR PRINTS; PR00196; ANNEXIN.
DR ProDom; PD000143; Annexin; 8.
DR SMART; SMO0335; ANX; 8.
DR PROSITE; PS00223; ANNEXIN; 7.
KW Annexin; Calcium/phospholipid-binding; Repeat.
FT INTR_MET 0 0
FT BY SIMILARITY.

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FT REPEAT 28 88 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
SQ SEQUENCE 672 AA; 75622 MW; BBET798A9CAB1511 CRC64;

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Query Match 58.2%; Score 931; DB 1; Length 672;
 Best Local Similarity 59.0%; Pred. No 4e-53;
 Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;

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QY 6 RGVTVTPGFEDEBADAETLRKAMKGLGTDSEITLTLSRSNAQROEISAFTLFGRL 65
D 10.RGVTVDPADPDANQDAEALVTANKGSGDSLEILTSNNQROEICQYSLSVGLK 69
QY 66.LDDLKSELTKFEKLIIVALKMPSRLVDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 125
D 70.IADLKELTKGFEKRLIVNMRPLAYCDAKEIKDAISGIGTDEKCLIEIIASRTPEELRAI 129
QY 126.QVVEEYSSSLDDVDVGTSGYQMLVYLQANRDPDAGIDEAQVEDQAALFQAGEL 185
D 130.VAAYKDAYERDESIIIGDTSGFQMLVLLQGTRENDVVSSEDLVQDDVQDLYEAGEL 189
QY 186.KMGTDSEKFTITFGTSVSHLRKVPDKWMTISGFQIEETIDETSQNLQOLLAVYKSI 245
D 190.KMGTDSEKFTITFGTSVSHLRKVPDKWMTISGFQIEETIDETSQNLQOLLAVYKSI 249
QY 246.SIPAYLAETLYYAMKAGTDHTLIRVWVSREIDLPNIRKFRKQNPATSLYSMTKGDTS 305
D 250.STPEYFAERLYKSMKGLGTDNTLIRVWVSRAEIMDMIRANFKLYGKSLYSFTKGDTS 309
QY 306.GDYKXALLLCGEDD 320
D 310.GDYKXALLLCGEDD 324

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RESULT 11

ANK6_HUMAN STANDARD; PRT: 672 AA.

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AC P08133;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III)
DE (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CP3-II).
GN ANX6 OR ANX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88124902; PubMed=2963335;
RA Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.;
RT "Human 67-kDa calelectrin contains a duplication of four repeats
RT found in 35-kDa lipocortin."
RL Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=89380132; PubMed=2528541;
RA Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T.,
RA Saino Y., Shidara Y., Maki M.;

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RT "Structure and expression of cDNA for calphobindin II, a human
RT placental coagulation inhibitor.";
RL J. Biochem. 106:43-49 (1989).
RN [4]
RN SEQUENCE.
RX MEDLINE=90236978; PubMed=2139657;
RA Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
RA Makai M.;
RT "Structure and properties of calphobindin II, an anticoagulant
RT protein from human placenta.";
RL J. Biochem. 107:43-50 (1990).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS):
RX MEDLINE=96326697; PubMed=8709144; Demange P., Goettig P., Liemann S.,
RA Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann S.,
RA Huber R., Voges D.;
RT "The structure of recombinant human annexin VI in crystals and
RT membrane-bound";
RL J. Mol. Biol. 260:638-643 (1996).
CC -1- FUNCTION: May associate with CD21. May regulate the release of
CC Ca(2+) from intracellular stores.
CC -1- INDUCTION: By EBV.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- PTM: Phosphorylated in response to growth factor stimulation.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 8 annexin repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00510; BAA00400.1; -;
DR EMBL: Y00097; CA68286.1; -;
DR EMBL: J03578; AAA35636.1; -;
DR EMBL: BC017046; AAH17046.1; -;
DR PIR: J00032; ACHU68.
DR PDB: 1M91; 15-APR-03.
DR Genew: HGNC:544; ANXA6.
DR MIM: 114070; -;
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin; 8.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; Annexin; 8.

DR SMART, SM00335; ANX; 8.
DR PROSITE, PS00223; ANNEXIN; 8.
KW Annexin; Calcium/phospholipid-binding; Repeat; Acetylation;
KW phosphorylation; 3D-structure.
FT INIT_MET 0
FT REPEAT 28 8 ANNEXIN 1.
FT REPEAT 100 160 ANNEXIN 2.
FT REPEAT 184 244 ANNEXIN 3.
FT REPEAT 259 319 ANNEXIN 4.
FT REPEAT 371 431 ANNEXIN 5.
FT REPEAT 443 503 ANNEXIN 6.
FT REPEAT 532 592 ANNEXIN 7.
FT REPEAT 607 667 ANNEXIN 8.
FT MOD_RES 1 1 ACETYLATION.
FT REPEAT 225 226 IE -> MK (IN REF. 2).
FT CONFLICT 554 554 S -> T (IN REF. 2).
FT CONFLICT 618 618 E -> D (IN REF. 1).
SQ SEQUENCE 672 AA; 75742 MW; 2829237029BDIDCB CRC64;

Query Match 57.9%; Score 927; DB 1; Length 672;
Best Local Similarity 57.8%; Pred. No. 7.2e-53;
Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;

QY 6 RGTVDPPGDEDRADAEITLRKAMKGLGTDSEIILTLTSRSNAQROEISAFKTLFGRL
DB 10 RSHIDFPQDPDNOQDEALYTKMGFGSDKEALIDITTSRSRQROQVOCQSYLSYKTK
QY 66 LDDKSELTKPEKTLVALLMKPSRLYDAVELKHALKAGTNGKVLTEIISRTPPEELRR
DB 70 IADLKELTKGERLVLGMRPAVCDAKEIDALSGITDEKCLIEIASLTNEQMH
QY 126 KQVEEYESSLEDDVVGDTSGYQRMVLLQANRPDAGIDEAVEODALFOAG
DB 130 VAAVDAVRDEADLIIGTSHQPMVLVLLQGTREDDVSEDLVQDDVDLYEAG
QY 186 KNGTDEKFTTIGTRSVSHLRKVPDKYTWITSGFOIEITIDETSGNLEQOLLAVKKS
DB 190 KNGTDEAQFIYILGNRSKQHLRLVPEYELTKTGKPIEASIRBELSGDFEKLMLAAVKK
QY 246 SIPATIAETLYYAMGAGTDHDTLLRWVMSRSEIDLFINRKERKNFATSLYSMIGD
DB 250 STPEYFAERLFRAMKGLGTRDWTLLRIWVSRSELDLIRELFRYKSLYSIMKND
QY 306 GDYKATLLTGCEDD 320
DB 310 GEYKTKLTKSGDD 324

RESULT 12
ANX4_MOUSE STANDARD; PRT; 318 AA.
ID ANX4_MOUSE
AC P97429;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Annexin A4 (Annexin IV).
GN ANXA4 OR ANXA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RA Sable C.L., Shannon J., Riches D.W.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (by similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the annexin family.

```

CC -!- SIMILARITY: Contains 4 annexin repeats.
CC
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CC
CC EMBL: U72941; AAB40697.1; -.
CC HSSP: P13214; IANN.
CC MGD: MGI:88030; Anxa4.
CC InterPro: IPR001464; Annexin.
CC Pfam: PF00191; annexin; 4.
CC PRINTS: PR00196; ANNEXIN.
CC ProDom: PD000143; Annexin; 4.
CC SMART: SM00335; ANX; 4.
CC PROSITE: PS00223; ANNEXIN; 4.
CC Annexin; Calcium/phospholipid-binding; Repeat.
CC INIT MET 0 0 ANNEXIN 1.
CC REPEAT 22 82 ANNEXIN 1.
CC REPEAT 94 154 ANNEXIN 2.
CC REPEAT 178 238 ANNEXIN 3.
CC REPEAT 253 313 ANNEXIN 4.
CC SEQUENCE 318 AA; 35858 MW; 53FAC7AD8006BCD CRC64;

Query Match 57.9%; Score 926; DB 1; Length 318;
Best Local Similarity 57.6%; Pred. No. 3.4e-53;
Matches 181; Conservative 58; Mismatches 75; Indels 0; Gaps 0;

QY 7 GTVTDFPEFDRADDELTKAMKKGCTDEESILLTTSRSNAOROETSAFETLFGRL 66
Db 5 GTVRAASFNATEDQTLRKMKKGCTDEDMIGLAVRNTRQREIRSAVSTIGRLI 64
QY 67 DDLKSELGKEFKLVALMKPSRLYDAVELKHALKGATNKEVLEIISAPTEELRAIK 126
Db 65 EDLSELSNFEQVILGIMPTVLYDVELRKAMKGAGTDEGLIEIASRTPERIRIN 124
QY 127 QVVEERYSSLEDDVVGDTSGGYQRMVLLQANRDPDAGIDEAQVEQDAQFLPQAGELK 186
Db 125 QTYQQQYGRSLIEDICSDTSPFMQFVLFSLAAGRDESNYDDMLMKQDAQLVEAGSKR 184
QY 187 WGTDEBEKRTTIGTRSVSHLKKVPDKYWTISGFOIETITDETSNTLEQLIAVKSIRS 246
Db 185 WGTDEVKFLSTLCGRNRNHLHVEPEYKRIQKIDEGIKSETSGSFEDALLAIVKQRS 244
QY 247 IPATLAETLYAMGAGTDDHTLIRVWVSRSEIDLFNIRKPKKFAISLYEMIKGDTSG 306
Db 245 KPSYFAERLYKSMGLGTDNTLIRVWVSRSEIDLIRASFKRLYGRSLYEFIKGDTSG 304
QY 307 DYKKAALLLCGEDD 320
Db 305 DYRKVLILCGDD 318

RESULT 13
ANXA_BOVIN STANDARD: PRT; 318 AA.
ID ANXA_BOVIN STANDARD: PRT; 318 AA.
AC P13214;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A4 (Annexin IV) (lipocortin IV) (Endomexin I) (Chromobindin 4)
DE (Protein II) (P32.5) (placental anticoagulant protein II) (PAP-II)
DE (P34-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41)
DE (P33/41).
GN ANXA4 OR ANXA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;

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```

RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=89050088; PubMed=2847715;
RA Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
RT "Cloning and characterization of a cDNA encoding bovine endomexin
RT (chromobindin 4).";
RL Biochem. Biophys. Res. Commun. 156:660-667(1988).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96205957; PubMed=8631806;
RA Kojima K., Yamamoto K., Irimura T., Ogawa T., Ogawa H., Matsumoto I.;
RT "Characterization of carbohydrate-binding protein p33/41: relation
RT with annexin IV, molecular basis of the doublet forms (p33 and p41),
RT and modulation of the carbohydrate binding activity by
RT phospholipids.";
RL J. Biol. Chem. 271:7679-7685(1996).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sutton R.B., Sprang S.R.;
RL Submitted (SEP-1995) to the PDB data bank.
RN [4]
RN X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=98070213; PubMed=9405281;
RA Zanotti G., Malpeli G., Glubich F., Folli C., Scopini M., Olivieri L.,
RA Savoia A., Berni R.;
RT "Structure of the trigonal crystal form of bovine annexin IV.";
RL Biochem. J. 329:101-106(1998).
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- MISCELLANEOUS: Seems to bind one calcium ion with high affinity.
CC -!- SIMILARITY: Belongs to the annexin family.
CC -!- SIMILARITY: Contains 4 annexin repeats.
CC
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CC
CC EMBL: M22248; AAA30507.1; -.
CC EMBL: X13627; CAA31954.1; -.
CC EMBL: D78178; BAA11243.1; -.
CC PIR: A31578; LUBO4.
CC PDB: 1ANN; 29-JAN-96.
CC PDB: 1AOW; 14-JAN-98.
CC PDB: 1I4A; 25-APR-01.
CC InterPro: IPR001464; Annexin.
CC Pfam: PF00191; annexin; 4.
CC PRINTS: PR00196; ANNEXIN.
CC ProDom: PD000143; Annexin; 4.
CC SMART: SM00335; ANX; 4.
CC PROSITE: PS00223; ANNEXIN; 4.
CC Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure.
CC INIT MET 0 0 ANNEXIN 1.
CC REPEAT 22 82 ANNEXIN 1.
CC REPEAT 94 154 ANNEXIN 2.
CC REPEAT 178 238 ANNEXIN 3.
CC REPEAT 253 313 ANNEXIN 4.
CC CONFLICT 94 94 L -> V (IN REF. 2).
CC CONFLICT 210 210 E -> K (IN REF. 2).
CC HELIX 15 26
CC HELIX 33 40
CC HELIX 41 42
CC HELIX 45 59
CC HELIX 63 70
CC HELIX 73 83
CC HELIX 86 98
CC HELIX 105 114
CC HELIX 117 131

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FT HELIX 135 142
 FT HELIX 145 155
 FT TURN 156 156
 FT HELIX 167 182
 FT TURN 183 185
 FT HELIX 189 198
 FT HELIX 201 215
 FT HELIX 219 226
 FT HELIX 229 257
 FT TURN 264 274
 FT HELIX 275 278
 FT HELIX 279 290
 FT HELIX 294 301
 FT HELIX 304 314
 SQ SEQUENCE 318 AA; 35757 MW; 86BDBDF349D774FD CRC64;

Query Match 57.8%; Score 924; DB 1; Length 318;
 Best Local Similarity 58.3%; Pred. No. 4,6e-53;
 Matches 183; Conservative 51; Mismatches 80; Indels 0; Gaps 0;

QY 7 GTVTDPGDERADAEFLTKRANKGLGTDSEITLTLSRSNMQROEISAFTLFGDRL 66
 DB 5 GTVKAAGFNAAEDAGTLRKANKGLGTDDEDAITVLAISTAOKEITRTAYKTIGRDL 64
 QY 67 DDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVTETIIASRPEELRAIK 126
 DB 65 DDLKSELTSNFEQVILGMITPTLVLYVOELRKANKAGDEGLIILASRPEELIRLN 124
 QY 127 QVVEEYSGSLIEDVVDGTSYQRMVYLQANRPDAGIDEAQQEQAALFOAGEIK 186
 DB 125 QTYOLOYGRSLEDDISDTSFMQGVLSLSAGGRDESNVLDALMKQDQADLYEAGEKK 184
 QY 187 WGTDEEKFTITFTRSVSHLRKVFYKMYTISGFQIETTIRETSNLEQLLAVVSIS 246
 DB 185 WGTDEVKFLTVLCSSRNHLLHVFDEYKRIAQKIDIEGISEFTSGSFEDLLAIIVCMRN 244
 QY 247 IPAYLAETLYANKAGCTDHTLIRVWVSSEIDLPRIKEPKNFATSLYSMIKGTSG 306
 DB 245 KSAVFARLYKSMKGLGTDITLIRVWVSRAEIDMDIRANFKLYGKSLYSFIKGTSG 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYKRVLLILCGGD 318

RESULT 14

ANX4 CANFA STANDARD; PRT; 318 AA.
 ID ANX4 CANFA
 AC P50994;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Annexin A4 (Annexin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
 GN ANX4 OR ANX4.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N. A., AND SEQUENCE OF 78-95 AND 134-149.
 RC STRAIN=Mongrel; Tissue=Pancreas;
 RX MEDLINE=22015264; PubMed=12020832;
 RA Fukuoaka S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.,
 RT "Cloning and characterization of ZAP36, an annexin-like, zymogen granule membrane associated protein, in exocrine pancreas.",
 RL Biochim. Biophys. Acta 1575:148-152(2002).
 RN [2]
 RP SEQUENCE OF 1-9.
 RX MEDLINE=94362286; PubMed=7765250;
 RA Fukuoaka S.-I.,
 RT "Analysis of ZAPs, zymogen granule membrane associated proteins, in the regulated exocytosis of the pancreas.",

RL Biosci. Biotechnol. Biochem. 58:1282-1285(1994).
 CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis (By similarity).
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
 CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity (By similarity).
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.

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DR EMBL; D13823; BAA07398.1; -.
 DR HSRP; P13214; IANM.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PR00196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 DR Annexin; Calcium/phospholipid-binding; Repeat.
 KW INIT MET 0
 FT REPEAT 22 82 ANNEXIN 1.
 FT REPEAT 94 154 ANNEXIN 2.
 FT REPEAT 178 238 ANNEXIN 3.
 FT REPEAT 253 313 ANNEXIN 4.
 FT CONFLICT 138 138 V -> D (IN REF. 1; AA (SEQUENCE)).
 SQ SEQUENCE 318 AA; 35681 MW; 42EF5B89179B4863 CRC64;

Query Match 56.9%; Score 911; DB 1; Length 318;
 Best Local Similarity 57.3%; Pred. No. 3.2e-52;
 Matches 180; Conservative 54; Mismatches 80; Indels 0; Gap

QY 7 GTVTDPGDERADAEFLTKRANKGLGTDSEITLTLSRSNMQROEISAFTLFGDRL 66
 DB 5 GTVKAAGFNAAEDAGTLRKANKGLGTDDEDAITVLAISTAOKEITRTAYKTIGRDL 64
 QY 67 DDLKSELTKGFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVTETIIASRPEELRAIK 126
 DB 65 DDLKSELTSNFEQVILGMITPTLVLYVOELRKANKAGDEGLIILASRPEELIRLN 124
 QY 127 QVVEEYSGSLIEDVVDGTSYQRMVYLQANRPDAGIDEAQQEQAALFOAGEIK 186
 DB 125 QTYOLOYGRSLEDDISDTSFMQGVLSLSAGGRDESNVLDALMKQDQADLYEAGEKK 184
 QY 187 WGTDEEKFTITFTRSVSHLRKVFYKMYTISGFQIETTIRETSNLEQLLAVVSIS 246
 DB 185 WGTDEVKFLTVLCSSRNHLLHVFDEYKRIAQKIDIEGISEFTSGSFEDLLAIIVCMRN 244
 QY 247 IPAYLAETLYANKAGCTDHTLIRVWVSSEIDLPRIKEPKNFATSLYSMIKGTSG 306
 DB 245 KSAVFARLYKSMKGLGTDITLIRVWVSRAEIDMDIRANFKLYGKSLYSFIKGTSG 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYKRVLLILCGGD 318

RESULT 15

ANX6 CHICK STANDARD; PRT; 671 AA.
 ID ANX6 CHICK
 AC P51901;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Annexin A6 (Annexin VI) (lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20) (67 kDa catelectrin) (Calphobindin-II) (CPB-II).

[illegible]

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Db          306 DTSGEYKRLKLCGDD 324
          |||:|||||:|:|:|
RESULT 16
ANXA RAT
ID ANXA RAT          STANDARD:      PRT;      318 AA.
AC P55260;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule
DE membrane associated protein) (ZAP36).
OS ANXA4 OR ANXA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
(1)
SEQUENCE FROM N.A.
RP STRAIN=Mistar; TISSUE=Pancreas;
RC MEDLINE=22015264; Pubmed=12020832;
RX Fukuoka S.-I., Horst K., Kazuki-Sugino R., Ikeda Y.;
RA "Cloning and characterization of ZAP36, an annexin-like, zymogen
RT granule membrane associated protein, in exocrine pancreas.";
RL Biochim. Biophys. Acta 1575:148-152(2002).
CC -1- FUNCTION: Calcium/phospholipid-binding protein which promotes
CC membrane fusion and is involved in exocytosis (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- MISCELLANEOUS: Seems to bind one calcium ion with high affinity
CC (by similarity).
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
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-----
CC DR EMBL; D38224; BAA07399.2; -.
CC .DR HSSP; P13214; IAN.
CC DR InterPro; IPR001464; Annexin.
CC Pfam; PF00191; annexin.4.
CC PRINTS; PR00196; ANNEXIN.
CC ProDom; PD000143; Annexin; 4.
CC SMART; SM00335; ANX; 4.
CC DR PROSITE; PS00223; ANNEXIN; 4.
CC KW Annexin; Calcium/phospholipid-binding; Repeat.
CC FT INIT_MET 0
CC FT REPEAT 22 82 BY SIMILARITY.
CC FT REPEAT 94 154 ANNEXIN 1.
CC FT REPEAT 178 238 ANNEXIN 2.
CC FT REPEAT 253 313 ANNEXIN 3.
CC FT REPEAT 318 AA; 35717 MW; FF630ABEA22ED2E7 CRC64;
SQ SEQUENCE
Query March 56.4%; Score 903; DB 1; Length 318;
Best local similarity 56.7%; Pred. No. 1.1e-51;
Matches 178; Conservative 54; Mismatches 82; Indels 0; Gaps 0;
QY 7 GTVTDPPGPDERAETLRKAMKGLGTDESSITLTLLTSRNAORISAFKTLFGDGL 66
QY 5 GTVKAASGFATIEDAQLVRKAMKGLGTDEDAITGLVLCRNTAQRQRETRTYKSTIGDGL 64
QY 67 DDIKSELTKGEFKLIVALKMPSRLYDAYELDKALKGAGTNEKVLTEIIASRTPEELRAIK 126
QY 65 EDIKSELTSNFEQVILGMMPVTLVYQELRRAMKAGTDEGCLIELASRNPEIRIN 124
QY 127 QVVEEYSGSLLEDVDVGTDSYGYQRMLVVLQANRPDAGIDPAQVEQDAALFQAGELK 186

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CC -!- SIMILARITY: Contains 4 annexin repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10883; BAA01705.1; -.
DR PIR: JH0694; LURB11.
DR HSSP: P13214; IANW.
DR GO: GO:0005635; C:nuclear membrane; ISS.
DR GO: GO:0005654; C:nucleoplasm; ISS.
DR GO: GO:0005515; F:protein binding; ISS.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin.4.
DR PRINTS: PR00196; Annexin.
DR ProDom: PD000143; Annexin.4.
DR SMART: SMO0335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KM Annexin; Calcium/phospholipid-binding; Repeat.
FT REPEAT 207 267 ANNEXIN 1.
FT REPEAT 279 339 ANNEXIN 2.
FT REPEAT 363 423 ANNEXIN 3.
FT REPEAT 438 498 ANNEXIN 4.
SQ SEQUENCE 503 AA; 54034 MW; 44C15F290770AC9F CRC64;

Query Match 54.6%; Score 873; DB 1; Length 503;
Best Local Similarity 54.6%; Pred. No. 1,6e-49;
Matches 172; Conservative 60; Mismatches 83; Indels 0; Gaps 0;

QY 6 RGVYDFGPEPERADAEFLTRAMKGLGDEESILTLTSSNAQROEISAAFKTLFGEDL 65
DB 189 RGTITDASGPDPLRDAEVLRAKMGCGFTDEQAIIDCGSRNKQOQLLFKAYGKDL 248
QY 66 LDDLKSELTGFEKILVLMKPSRLVAYELKALKAGKGTNEKVTETIASRTPEELRAI 125
DB 249 IKDKSELSGNFEKILVLMKPSRLVAYELKALKAGKGTNEKVTETIASRTPEELRAI 308
QY 126 KQVVEEYSGSLLEDVAGDTSGYVQRMVLVLOANRDPDAGIDEQVQDQCALFQAGEL 185
DB 309 NKAKTEKTEKTLERISDTSGHFQRLTISQGRDSTVDMSLVQDVCETVYAGEN 368
QY 186 KMGDEEKFITIFGRSVSHRKVYDKYMTISGQIETITRETSGNLEOLLVAVSIR 245
DB 369 RLGTDESKFNANVLCSRAHVAVFNEYQRMGTGRDIKESICREWSGDLQGMILVVKCLK 428
QY 246 SIPAYLAETLYAMKAGTDDHTLIRVWSRSEIDLFNIRKPEKFNATSLYSMIKQDTS 305
DB 429 NTPAFPAERLRNARMGAGTKRITLIRVWSRSEIDLDIRAEYKRMYSKSLYHISQDTS 488
QY 306 GDYKALILLGCEDD 320
DB 489 GDYRKILLIKICGND 503

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RP SEQUENCE FROM N.A.
RC TISSUB=Teratocarcinoma;
RX MEDLINE=94140847; PubMed=7508441;
RA Misaki Y., Pruin G.J.M., van der Kemp A.W., van Venrooij W.J.;
RT "The 56K autoantigen is identical to human annexin XI."
RL J. Biol. Chem. 269:4240-4246(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469408; PubMed=11013079;
RA Barces P., Fernandez M.R., Rodriguez-Garcia M.I., Morgan R.O.,
RA Fernandez M.P.;
RT "Annexin AII (ANXA11) gene structure as the progenitor of paralogous
RT annexins and source of orthologous cDNA isoforms."
RL Genomics 69:95-103(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUB=Lymph;
RX MEDLINE=12477932; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe U.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND POSSIBLY NUCLEAR.
CC -!- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -!- DISEASE: Antibodies against ANXA11 are present in sera from
CC patients with various autoimmune diseases, predominantly in sera
CC from patients with rheumatoid arthritis, systemic lupus
CC erythematosus, or Sjogren's syndrome.
CC -!- SIMILARITY: Belongs to the annexin family.
CC -!- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC -----
DR EMBL: L19605; AAA19734.1; -.
DR EMBL: AJ278463; CAB94995.1; -.
DR EMBL: AJ278464; CAB94996.1; -.
DR EMBL: AJ278465; CAB94997.1; -.
DR EMBL: BC007564; AA07564.1; -.
DR PIR: A53152; A53152.
DR HSSP: P13214; IANW.
DR Genew: HGNC:535; ANXA11.
DR MIM: 602572; -.
DR GO: GO:0005737; C:cytoplasm; TAS.
DR GO: GO:0005635; C:nuclear membrane; NAS.
DR GO: GO:0005654; C:nucleoplasm; NAS.
DR GO: GO:0005543; F:phospholipid binding; TAS.
DR GO: GO:0005515; F:protein binding; IPT.
DR GO: GO:0006955; P:immune response; TAS.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin.4.

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RESULT 19
ANXB_HUMAN
ID ANXB_HUMAN STANDARD; PRT; 505 AA.
AC P50995;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAF-50)
DE (56 kDa autoantigen).
GN ANXA11 OR ANX11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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PRINTS: PRO0196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat; Polymorphism.
 FT REPEAT 209 269 ANNEXIN 1.
 FT REPEAT 281 341 ANNEXIN 2.
 FT REPEAT 365 425 ANNEXIN 3.
 FT REPEAT 440 500 ANNEXIN 4.
 FT VARIANT 230 230 R -> C (in dbSNP:1049550).
 FT VARIANT 457 457 /FTID=VAR_012006.
 FT VARIANT 457 457 I -> V (in dbSNP:1802932).
 FT VARIANT 457 457 /FTID=VAR_012007.
 SQ SEQUENCE 505 AA; 54389 MW; 4ADCAC9F270BEE4 CRC64;
 Query Match 54.1%; Score 865; DB 1; Length 505;
 Best Local Similarity 53.7%; Pred. No. 5,3e-49;
 Matches 169; Conservative 61; Mismatches 85; Indels 0; Gaps 0;
 QY 6 RGTVDTPGDFERADAEETLRKAMKGLTDEESITLTLTSRSNAORQISAAFTLFGRL 65
 DB 191 RGTITDAPGDFDPRDAEVLRLKAMKGGTDEQALIDCLSSRSNKQROQILSTFKYAGKL 250
 QY 66 LDDIKSELTKGPEKLVIAIMKPSRLVDAYELKHALKGAGNEKVLTEIIASRTPEELRAI 125
 DB 251 IKDLKSELGNEFKETLALMKTPVLPDIYEIKALKIGVGTDEACLEIILASRNEHIREL 310
 QY 126 KQVEEYEGSSLEDVVGDTSGYGYORMLVLLQANRDPAGIDEAEOVDAQALFOAGEL 185
 DB 311 NPAVKAEPKKTLEAARSDTSGHFQRLILSLSGNDESNVMSLAQRDQALVYAAGN 370
 QY 186 KMGTEDEEFTITFGTRSVSHLRKVFDPKXMTISGFOIETIDRETSGNLEQLLAVYKSR 245
 DB 371 RIGTDESKFNALVLCSSRAHLVAVFNEYQMTGRDIEKSCIRMSGDLLEGMLAVVCKLK 430
 QY 246 SIPAVLAETLYYANKAGTDDHTLIRVMSRSSEIDLFNIRKERRKFNATSLYSMTIGDS 305
 DB 431 NTPAFPAERLNMKMRGAGTDRILIRVMSRSSEIDLFNIRSEYKMYGKSLYHDISGDT 490
 QY 306 GDYKALLLCEGDD 320
 DB 491 GDYRKILKICGGND 505
 RESULT 20
 ANXB MOUSE STANDARD; PRT; 503 AA.
 AC P97384;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP-50).
 GN ANXA11 OR ANXA11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97092887; PubMed=6938449;
 RA Fernandez M.P., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RT "Sequence and chromosomal localization of mouse annexin XI";
 RL Genomics 37:366-374(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=20469408; PubMed=11013079;
 RA Bances P., Fernandez M.R., Rodriguez-Garcia M.I., Morgan R.O.,
 RT "Annexin A11 (ANXA11) gene structure as the progenitor of paralogous
 RT Genomics 69:95-103(2000)."

CC -1- FUNCTION: Binds specifically to calcyclin in a calcium-dependent
 CC manner.
 CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
 CC calcium and phospholipid.
 CC -1- SIMILARITY: Belongs to the annexin family.
 CC -1- SIMILARITY: Contains 4 annexin repeats.
 CC -----
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 CC -----
 DR EMBL; U65986; AAB42012.1; -
 DR EMBL; AJ289760; CAB94770.1; -
 DR EMBL; AJ289761; CAB94770.1; JOINED.
 DR EMBL; AJ289762; CAB94770.1; JOINED.
 DR EMBL; AJ289763; CAB94770.1; JOINED.
 DR EMBL; AJ289764; CAB94770.1; JOINED.
 DR EMBL; AJ289765; CAB94770.1; JOINED.
 DR EMBL; AJ289766; CAB94770.1; JOINED.
 DR EMBL; AJ289767; CAB94770.1; JOINED.
 DR EMBL; AJ289768; CAB94770.1; JOINED.
 DR EMBL; AJ289769; CAB94770.1; JOINED.
 DR HSSP; P13214; IANN.
 DR SWISS-2DPAGE; P97384; MOUSE.
 DR MGJ; MG108481; Anxa11.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005654; C:nucleoplasm; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR InterPro; IPR001464; Annexin.
 DR Pfam; PF00191; annexin; 4.
 DR PRINTS; PRO0196; ANNEXIN.
 DR ProDom; PD000143; Annexin; 4.
 DR SMART; SM00335; ANX; 4.
 DR PROSITE; PS00223; ANNEXIN; 4.
 KW Annexin; Calcium/phospholipid-binding; Repeat.
 FT REPEAT 207 267 ANNEXIN 1.
 FT REPEAT 279 339 ANNEXIN 2.
 FT REPEAT 363 423 ANNEXIN 3.
 FT REPEAT 438 498 ANNEXIN 4.
 SQ SEQUENCE 503 AA; 54111 MW; 424B1345E0F4EC8A CRC64;
 Query Match 53.6%; Score 857; DB 1; Length 503;
 Best Local Similarity 54.0%; Pred. No. 1.7e-48;
 Matches 170; Conservative 59; Mismatches 86; Indels 0; Gap
 QY 6 RGTVDTPGDFERADAEETLRKAMKGLTDEESITLTLTSRSNAORQISAAFTLFGRL 65
 DB 189 RGTITDAPGDFDPRDAEVLRLKAMKGGTDEQALIDCLSSRSNKQROQILSTFKYAGKL 250
 QY 66 LDDIKSELTKGPEKLVIAIMKPSRLVDAYELKHALKGAGNEKVLTEIIASRTPEELRAI 125
 DB 249 IKDLKSELGNEFKETLALMKTPVLPDIYEIKALKIGVGTDEACLEIILASRNEHIREL 310
 QY 126 KQVEEYEGSSLEDVVGDTSGYGYORMLVLLQANRDPAGIDEAEOVDAQALFOAGEL 185
 DB 309 SRAVKTFQKTLERAIASDTSGHFQRLILSLSGNDESNVMSLAQRDQALVYAAGN 370
 QY 186 KMGTEDEEFTITFGTRSVSHLRKVFDPKXMTISGFOIETIDRETSGNLEQLLAVYKSR 245
 DB 369 RIGTDESKFNALVLCSSRAHLVAVFNEYQMTGRDIEKSCIRMSGDLLEGMLAVVCKLK 430
 QY 246 SIPAVLAETLYYANKAGTDDHTLIRVMSRSSEIDLFNIRKERRKFNATSLYSMTIGDS 305
 DB 429 NTPAFPAERLNMKMRGAGTDRILIRVMSRSSEIDLFNIRSEYKMYGKSLYHDISGDT 490
 QY 306 GDYKALLLCEGDD 320
 DB 489 GDYRKILKICGGND 503

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RESULT 21
ANX8_MOUSE STANDARD; PRT; 327 AA.
ID ANX8_MOUSE 035640;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Annexin A8 (Annexin VIII).
GN ANX8 OR ANX8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Fetal;
RX MEDLINE=96096578; PubMed=9434938;
RA Fernandez M.P., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Morgan R.O.;
RT "The genetic origin of mouse annexin VIII.";
RL Mamm. Genome 9:8-14(1998).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade (By similarity).
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ002390; CAA05364.1;
DR HSP: P14668; 1A8B.
DR MGD: MGI:1201374; Anx8.
DR InterPro: IPR001464; Annexin.
DR Pfam: PF00191; annexin.4.
DR PRINTS: PR00196; ANNEXIN.
DR ProDom: PD000143; ANNEXIN.4.
DR SMART: SM00335; ANX; 4.
DR PROSITE: PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation.
FT REPEAT 38 ANNEXIN 1.
FT REPEAT 110 162 ANNEXIN 2.
FT REPEAT 195 247 ANNEXIN 3.
FT REPEAT 270 322 ANNEXIN 4.
SQ SEQUENCE 327 AA; 36843 MW; 2CC6163642D29E8A0 CRC64;

Query Match 52.7%; Score 842.5; DB 1; Length 327;
Best local similarity 57.2%; Pred. No. 9e-48;
Matches 179; Conservative 49; Mismatches 84; Indels 1; Gaps 1;

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QY 247 IPAYLAETIYYAMKAGCTDHTLIRWVSRSEIDLFINRKEFRKGNFATSLYSMTKGTSG 306
DB 254 VHSYFAERLYYAMKAGCTRGDTLIRNIVSRSEIDLNIKQFRKGYKTLSSMTADTSG 313
QY 307 DYKALLILCGED 319
DB 314 YKRALNLVGTG 326

RESULT 22
ANX8_HUMAN STANDARD; PRT; 327 AA.
ID ANX8_HUMAN
AC P13928; Q9BTJ4;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A8 (Annexin VIII) (Vascular anticoagulant-beta) (VAC-beta).
GN ANX8 OR ANX8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90032687; PubMed=2530088;
RA Hauptmann R., Maurer-Fogy I., Krystek E., Bodo G., Andree H.,
RA Reutelingersperger C.P.W.;
RT "Vascular anticoagulant beta: a novel human Ca2+/phospholipid binding
RT protein that inhibits coagulation and phospholipase A2 activity. Its
RT molecular cloning, expression and comparison with VAC-alpha.";
RL Eur. J. Biochem. 185:63-71(1989).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92216091; PubMed=1313714;
RA Chang K.S., Wang G., Freireich E.J., Daly M., Maylor S.L.,
RA Trujillo J.M., Stas S.A.;
RT "Specific expression of the annexin VIII gene in acute promyelocytic
RT leukemia.";
RL Blood 79:1802-1810(1992).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shemen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: This protein is an anticoagulant protein that acts as an
CC indirect inhibitor of the thromboplastin-specific complex, which
CC is involved in the blood coagulation cascade.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----

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CC EMBL; X16662; CAA34650.1; -
 CC EMBL; M81844; AAB46383.1; -
 CC EMBL; BC004376; AAB04376.1; -
 CC EMBL; A07358; CAA00657.1; -
 CC PIR; S06476; LUNH8.
 CC HSSP; P14668; IBCZ.
 CC GENE; HGNC:546; ANXA8.
 CC MIM; 602396; -
 CC InterPro; IPR001464; Annexin.
 CC Pfam; PF00191; annexin; 4.
 CC PRINTS; PR00196; ANNEXIN.
 CC PRODOM; PD000143; Annexin; 4.
 CC SMART; SM00335; ANX; 4.
 CC PROSITE; PS00223; ANNEXIN; 4.
 CC Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
 CC Placenta; Polymorphism.
 CC REPEAT 30 ANNEXIN 1.
 CC REPEAT 102 ANNEXIN 2.
 CC REPEAT 187 ANNEXIN 3.
 CC REPEAT 262 ANNEXIN 4.
 CC VARIANT 6 A -> S.
 CC FTID-VAR 000604.
 CC Q -> T (IN REF. 2).
 CC F -> L (IN REF. 2).
 CC R -> S (IN REF. 2).
 CC A -> G (IN REF. 2 AND 3).
 CC GD -> RY (IN REF. 2).
 CC SEQUENCE 327 AA; 36879 MW; 3AAE1D7072A9379 CRC64;

Query Match 52.0%; Score 832.5; DB 1; Length 327;
 Best Local Similarity 56.5%; Pred. No. 4e-47;
 Matches 177; Conservative 48; Mismatches 87; Indels 1; Gaps 1;

QY 8 TVTDPGDFERRADAETLRKMKGLGDEESITLLTSSRNAQROEISAARETLFGRLD 67
 DB 14 TVKSSSHFNDDPAETLYKMKIGTNEQAIIDVLTQRSTQFOQIAKSFAGPKDLTE 73
 QY 68 DLKSELTGKREKTLVAMKPSRLYDAYELKHALKGAGNEVLTETIASRPEELRAIKQ 127
 DB 74 TLKSELGKFERLIVALMYPYRYEAKELHDMKGLGTEKEVILIELASRTKQDLREIMK 133
 QY 128 VYEEYGSLSLEDDVVGPTSGYVOMLVLLQANDP-DAGIDEAQVEQDAQALFOAGELK 186
 DB 134 AYEDYGSLSLEDDVVGPTSGYVOMLVLLQANDP-DAGIDEAQVEQDAQALFOAGELK 193
 QY 187 WGTDEEKPITLFGTSVSHLRKVPDKWITISGFOIEETIDRETSQNLLEAVKSI 246
 DB 194 RGTDEMKFTLLCTRSAHLRVEEYKANKSTEDSKETHSLEAMLVYKQCN 253
 QY 247 IPAYIAETLYYAMKAGTGDHLLIRVWVSRSEIDLFINRKEFRKNFATSLYMKIDTSG 306
 DB 254 LHSYFAERLYYAMKAGTGRDGLIRNIVSRSEIDLNLKCHPKKMYGKTLSSMIMEDTSG 313

QY 307 DYKKAALLLCGED 319
 DB 314 DYKKAALLLCGED 326

RESULT 23
 ANX3 HUMAN STANDARD; PRT; 323 AA.
 AC P12429;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedlin) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase).
 DE ANXA3 OR ANX3.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Carnivora; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88273202; PubMed=2968983;
 RA Pedinsky R.B., Tizard R., Mattaliano R.J., Sinclair L.K., Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.-S., Pratt D., Wachtel L., Hession C., Frey A.Z., Wallner B.P.;
 RT "Five distinct calcium and phospholipid binding proteins share homology with lipocortin I.";
 RL J. Biol. Chem. 263:10799-10811(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91301701; PubMed=1830024;
 RA Tait J.F., Frankenherry D.A., Miao C.H., Killary A.M., Adler D.A., Distche C.M.;
 RT "Chromosomal localization of the human annexin III (ANX3) gene.";
 RL Genomics 10:441-448(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94102764; PubMed=8276419;
 RA Tait J.F., Smith C., Xu L., Cookson B.T.;
 RT "Structure and polymorphisms of the human annexin III (ANX3) gene.";
 RL Genomics 18:79-86(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F., Diatchenko L., Marushta K., Farmer A.A., Rubin G.M., Hong L., Chappleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulvey S.J., Hosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Krzywicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.U.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 41-102 AND 126-138.
 RX MEDLINE=8918212; PubMed=2975506;
 RA Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T., Hendrickson L.E., Fujikawa K.;
 RT "Placental anticoagulant proteins: isolation and comparative characterization four members of the lipocortin family.";
 RL Biochemistry 27:6268-6276(1988).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=96229894; PubMed=8639653;
 RA Favier-Perron B., Lewit-Bentley A., Russo-Marie F.;

RT "The high-resolution crystal structure of human annexin III shows
RT subtle differences with annexin V." ;
RL Biochemistry 35:1740-1744(1996).
RN [8]
RP VARIANTS ASN-19; ASN-219; LEU-251 AND SER-291.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes." ;
RL Nat. Genet. 22:231-238(1999).
RN [9]
RP ERRATUM.
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -1- FUNCTION: Inhibitor of phospholipase A2, also possesses anti-
CC coagulant properties. Also cleaves the cyclic bond of inositol
CC 1,2-cyclic phosphate to form inositol 1-phosphate.
CC -1- DOMAIN: A pair of annexin repeats may form one binding site for
CC calcium and phospholipid.
CC -1- SIMILARITY: Belongs to the annexin family.
CC -1- SIMILARITY: Contains 4 annexin repeats.
CC -----
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CC -----
DR EMBL, M20560; AAA59496.1; -;
DR EMBL, M63310; AAA52284.1; -;
DR EMBL, L20591; AAA16713.1; -;
DR EMBL, BC000871; AAH00871.1; -;
DR PIR, A47658; LHMU3.
DR PDB, 1AXN; 08-MAR-96.
DR PDB, 1AII; 12-MAR-97.
DR SWISS-2DPAGE, P12429; HUMAN.
DR Aarhus/Ghent-2DPAGE, 5205; IEF.
DR PWMMA-2DPAGE, P12429; IEF.
DR Genew; HGNC:541; ANXA3.
DR MIM; 106490; -;
DR InterPro; IPR001464; Annexin.
DR Pfam; PF00191; annexin; 4.
DR PRINTS; PRO0196; ANNEXIN.
DR PRODOM; PD000143; Annexin; 4.
DR SMART; SM00335; ANX; 4.
DR PROSITE; PS00223; ANNEXIN; 4.
KW Annexin; Calcium/phospholipid-binding; Repeat;
KW Phospholipase A2 inhibitor; 3D-structure; Polymorphism.
FT REPEAT 27 87 ANNEXIN 1.
FT REPEAT 99 159 ANNEXIN 2.
FT REPEAT 183 243 ANNEXIN 3.
FT REPEAT 258 318 ANNEXIN 4.
FT VARIANT 19 19 S-> N (in dbSNP:5951).
FT VARIANT 219 219 /FTId=VAR 013914.
FT VARIANT 219 219 I-> N (in dbSNP:5948).
FT VARIANT 251 251 /FTId=VAR 013915.
FT VARIANT 251 251 P-> L (in dbSNP:5549).
FT VARIANT 291 291 /FTId=VAR 013916.
FT VARIANT 291 291 F-> S (in dbSNP:5941).
FT CONFLICT 146 146 /FTId=VAR 013917.
FT CONFLICT 294 294 S-> G (IN REF. 6).
FT TURN 4 5 H-> R (IN REF. 6).
FT TURN 16 17
FT HELIX 20 31

FT HELIX 38 45
FT TURN 46 47
FT HELIX 50 64
FT HELIX 68 75
FT HELIX 78 88
FT HELIX 91 103
FT HELIX 110 119
FT HELIX 122 136
FT HELIX 140 147
FT HELIX 150 160
FT TURN 161 162
FT HELIX 172 185
FT TURN 186 188
FT HELIX 194 203
FT HELIX 206 220
FT HELIX 224 231
FT HELIX 234 262
FT HELIX 269 279
FT TURN 280 283
FT HELIX 284 295
FT HELIX 299 306
FT HELIX 309 319
SQ SEQUENCE 323 AA; 36375 MW; 4128C715491FC132 CRC64;
Query Match 50.7%; Score 811; DB 1; Length 323;
Best Local Similarity 50.2%; Pred. No. 9.7e-46;
Matches 158; Conservative 61; Mismatches 96; Indels 0; Gaps 0;
QY 6 RGVTVDPGFGDERADAEFLRKAMKGLGTEDESILTLTSRSNAQROEISAFPLFGRLD 65
DB 9 RGVTVDPGFGDERADAEFLRKAMKGLGTEDESILTLTSRSNAQROEISAFPLFGRLD 68
QY 66 LDDLKSELGKFEKFLVAMKQPERLYDAYELKALKAGAGTNEKVLTEIIASRTPEELRAI 125
DB 69 KDILKSDLSGHEFHLVVALVTPPAVPDAKOLKSKMGAGTNEDELTEILTRTSRQMKOI 128
QY 126 KQYEEBEGSSLEDDVVDGTSGYQMLVYLQANDPDAGIDEADEVDAQALFQAGEL 185
DB 129 SQAYVTVYVKKSLGDDISSETSGDFRKLTLTLDGRDESLKYDEHLAKODAQILYKAGSN 188
QY 186 KMGTDKEKFLITGPRSVSHLRKVPKXMTTISGFQIEFTIDETSGNLEQOLLAVYKSTR 245
DB 189 KMGTDKEKFLITGPRSVSHLRKVPKXMTTISGFQIEFTIDETSGNLEQOLLAVYKSTR 248
QY 246 SIPAYLAETLYYAMKAGTDDHTLIRVWVSREIDLFNIRKEPRKNFATSLYSMIGDVS 305
DB 249 NTPAPLAEKLNHALKIGIGDEFTLNKRWVSREIDLFNIRKEPRKNFATSLYSMIGDVS 308
QY 306 GDYKALLLLCGEBD 320
DB 309 GDYEITLKKICGDD 323
RESULT 24
ANX3 MOUSE STANDARD; PRT; 323 AA.
ID ANX3 MOUSE
AC 035639;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant
DE protein III) (PAP-III) (35-alpha calcimedlin).
GN ANXA3 OR ANX3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=98172733; PubMed=9511742;
RA Fernandez M.P., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Morgan R.O.;

OS	Rattus norvegicus (Rat).	Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
ON	NCBI_TaxID=10116;	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=88273202; PubMed=2968983;	
RA	Pepinsky R.B., Tizard R., Matcaliano R.J., Sinclair L.K.,	
RA	Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,	
RA	Pratt D., Wachtler L., Hession C., Frey A.Z., Malner B.P.;	
RT	"Five distinct calcium and phospholipid binding proteins share	
RT	homology with lipocortin I."	
RL	J. Biol. Chem. 263:10799-10811(1988).	
CC	-1- FUNCTION: Inhibitor of phospholipase A2, also possesses anti-	
CC	coagulant properties.	
CC	-1- DOMAIN: A pair of annexin repeats may form one binding site for	
CC	calcium and phospholipid.	
CC	-1- SIMILARITY: Belongs to the annexin family.	
CC	-1- SIMILARITY: Contains 4 annexin repeats.	
CC	-----	
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CC	ration between the Swiss Institute of Bioinformatics and the EMBL outstc-	
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CC	use by non-profit institutions as long as its content is in i	
CC	modified and this statement is not removed. Usage by and for comm	
CC	entities requires a license agreement (See http://www.isb-sib.ch/annexin	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; M20559; AAAA1511.1; -	
DR	HSSP; P12429; IAXN.	
DR	InterPro; IPR001464; Annexin.	
DR	Pfam; PF00191; annexin; 4.	
DR	PRINTS; PR00196; ANNEXIN.	
DR	PRODom; PD000143; Annexin; 4.	
DR	SMART; SM00335; ANX; 4.	
DR	PROSITE; PS00223; ANNEXIN; 4.	
KW	Annexin; Calcium/phospholipid-binding; Repeat;	
KW	Phospholipase A2 inhibitor.	
FT	REPEAT 28 88 ANNEXIN 1.	
FT	REPEAT 100 160 ANNEXIN 2.	
FT	REPEAT 184 244 ANNEXIN 3.	
FT	REPEAT 259 319 ANNEXIN 4.	
FT	REPEAT	
SO	SEQUENCE 324 AA; 36322 MW; 5BAC42BAE32AE47 CRC64;	
QY	Query Match	48.88; Score 781; DB 1; Length 324;
QY	Best Local Similarity	48.38; Pred. No. 8.5e-44;
QY	Matches 152; Conservative 64; Mismatches 99; Indels 0; Gap	
Db	6 RGYTDPGPERADAEETLRKAMKGLGTDEESITLTLTSSNAOROEISAFAKTLFG	
Db	10 RGTNNVPGFNPVSADAEIRKALIGTDEKTLINILTERSNAOROLIVKHIGCAVEG	
QY	66 LDDIKSELITGFEKLIYALMKPRSLYDAYELKHALKAGNTEKYLTEIIASRTPEELF	
Db	70 KADLKGLDISGFENHWAMALITAPAVPFAKOLKSKMRGNGTDEDTLIELITRTSRQMK	
QY	126 KQYEEYSGSLEDVDVSGTSGYYQRMVLVLLQANRDPDAGIDEAQVQEQDAQALFOAC	
Db	130 SQAYTAAKKNLRDIDISSETSGDPRKALLTLADGGREBSLVDYDETLAKDQQTLYDAG	
QY	186 KMGTDSEKFTITFGTRSVSHLRKVPDKMTISGQIETIDRETSGNLEQALLAVKKS	
Db	190 KMGTDSEKFTIELCLRSPQDLTFDEYRNISQKDIEDISIGELSGHEDELLAVNR	
QY	246 STPAVLAETIYVAMGAGTDHITLIRVAVSRSEIDLFIRKFRFNKFNATSIYSMTKG	
Db	250 NTPPALAGRHQALGAGTDETTLNRIWVSRSEIDLLIRREFKKGHCSCISYSAIOS	
QY	306 GDYKALLLLCGEDD 320	
Db	310 GDYRTVLLKICGGD 324	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2004, 08:01:25 ; Search time 20 Seconds

(without alignments)
1539.064 Million cell updates/sec

Title: US-09-787-923-2

Perfect score: 1600

Sequence: 1 MAQVLRGTVTFPPFDERAD.....KQDTSGDYKALLLCGEDD 320

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1600	100.0	320	1 AOHUP	annexin V [validat
2	1545.5	96.6	320	1 S27214	annexin V - bovine
3	1464.5	91.5	319	1 LUR75	annexin V - rat
4	1289	80.6	321	1 LUCH5	annexin V - chicle
5	942	58.9	673	1 S01786	annexin VI - mouse
6	933	58.3	321	1 A42077	annexin IV - human
7	931	58.2	318	1 LUR64	annexin IV - pig
8	931	58.2	673	1 S52844	annexin VI - rat
9	927	57.9	673	1 AOHU68	annexin VI [valida
10	924	57.8	319	1 LUBO4	annexin IV - bovin
11	904.5	56.5	671	2 JC2029	annexin - chicken
12	875	54.7	503	1 LUBO11	annexin XI form A
13	875	54.7	505	1 S23447	annexin XI form B
14	873	54.6	503	1 LURB11	annexin XI - rabbi
15	865	54.1	505	2 A53152	annexin XI - huma
16	832.5	52.0	327	1 LURH8	annexin VII - huma
17	811	50.7	323	1 LURH3	annexin III - rat
18	785	49.1	324	1 LUR73	annexin VII, long
19	780	48.8	488	1 LURH7	annexin VII - mous
20	774	48.4	463	2 S29170	annexin XII - Hydr
21	716	44.8	316	1 LURF12	annexin XII - huma
22	708.5	44.3	339	1 LURH36	annexin VII - Afri
23	706	44.1	512	2 S70644	annexin VII - prote
24	704.5	44.0	676	2 S41022	annexin II - bovin
25	703.5	44.0	339	2 LUBO36	annexin II - rat
26	701.5	43.8	339	1 LUMS36	annexin II - mouse
27	692.5	43.3	341	1 S55277	annexin II - rat
28	688.5	43.0	340	1 UQ1298	annexin II type 2

30	685.5	42.8	340	1 JQ1287	annexin II type
31	681	42.6	296	1 LURF9	annexin IX - f
32	679	42.4	316	1 LURH15	annexin XIII,
33	679	42.4	321	1 LURF10	annexin X - fr
34	676.5	42.3	339	1 LUCH2	annexin II - c
35	671	41.9	316	2 AS7076	annexin XIIa
36	671	41.9	357	2 B57076	annexin I - gu
37	658	41.1	346	1 LUGP1	annexin I - hu
38	653	40.8	346	1 S28228	annexin I - bo
39	653	40.8	346	1 LUR71	annexin I - ra
40	642	40.1	346	1 A4118	annexin I type
41	634	39.6	346	1 LUMS1	annexin I - mo
42	588.5	36.8	322	2 B88452	annexin I type
43	581.5	36.3	322	2 S43578	annexin I type
44	540	33.8	317	2 LURP1	annexin I - Ra
45	538	33.6	462	1 LUD07	annexin VII -
46	529.5	33.1	316	2 S09020	annexin I - pig
47	511	31.9	157	2 A61507	annexin 2 - up
48	465.5	25.9	125	2 T10807	probable annex
49	414.5	25.9	315	2 T10807	probable annex
50	414	25.9	315	2 T06322	annexin - isofo
51	405.5	25.3	321	2 T06322	annexin - alfa
52	404	25.2	308	2 T09552	annexin - like
53	402.5	25.2	318	2 T50026	annexin - like
54	390.5	24.4	317	2 T02961	annexin - like
55	390	24.0	314	2 S66274	hypothetical
56	384.5	24.0	314	2 T50027	annexin P35 -
57	383.5	24.0	316	2 T25622	annexin homolo
58	383.5	23.1	351	2 T02975	annexin - upl
59	370	23.1	314	2 S56674	probable annex
60	369.5	22.6	271	2 T31428	annexin I - c
61	369.5	22.6	316	2 T10805	annexin homolo
62	349.5	21.6	315	2 H84808	annexin - upl
63	345.5	21.6	315	2 S08991	annexin - bo
64	345.5	21.6	134	2 S36103	alpha-2-giard
65	194.5	12.2	332	2 B26393	annexin II - c
66	189	11.8	86	2 A33735	myosin heavy
67	163.5	10.2	295	2 A60602	probable hist
68	123.5	7.7	36	2 A71969	probable ther
69	122.5	7.1	442	2 F71219	conserved hyp
70	113	6.9	549	2 F46440	ladder protei
71	109	6.8	74	2 T42223	thermosome, c
72	108.5	6.8	549	2 F75186	methyl-accept
73	108.5	6.7	678	2 E90059	ATP-dependent
74	107	6.7	701	2 A61231	heat-shock pr
75	106.5	6.7	546	2 E90205	myosin heavy
76	106.5	6.5	323	2 JC4770	conserved hyp
77	106.5	6.5	1023	2 A61280	hyperthermoph
78	106.5	6.4	1023	2 T33813	ATP-dependent
79	106.5	6.4	473	2 H97748	hypothetical
80	104.5	6.4	1440	2 G87838	hypothetical
81	104.5	6.3	1940	2 A24922	myosin heavy
82	104.5	6.3	1289	2 T31344	G880 precursor
83	103.5	6.3	1557	2 T18412	lipid-binding
84	103	6.3	1557	2 S55101	hypothetical
85	102.5	6.2	530	2 C87838	myosin heavy
86	102	6.2	551	2 T25197	protein T2361
87	101.5	6.2	1051	2 S59791	hypothetical
88	101	6.2	1051	2 A95031	probable memb
89	100	6.2	390	2 A11330	kinesin-like
90	100	6.2	617	2 G02157	hypothetical
91	100	6.2	617	2 A95031	prolyl-tRNA s
92	99.5	6.2	702	2 S59428	hypothetical
93	99.5	6.2	596	2 S57971	probable memb
94	99.5	6.2	2		apartic prot
95	99.5	6.2			
96	99.5	6.2			
97	99	6.2			
98	99	6.2			
99	99	6.2			
100	98.5	6.2			

ALIGNMENTS

RESULT 1:

AQHUP

Annexin V [validated] - human

N/Alternate names: endonexin II, lipocortin V, placental anticoagulant protein, placenta

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000

C/Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S06646; A29

R/Peptidase: R.B.; Tizard, R.; Maitellano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning,

J. Biol. Chem. 263, 10799-10811, 1988

A/Title: Five distinct calcium and phospholipid binding proteins share homology with lip

A/Reference number: A29659; PMID:88273202; PMID:2968983

A/Accession: D29250

A/Molecule type: mRNA

A/Residues: 1-320 <PEP>

A/Cross-references: GB:M1731; NID:g186969; PIDN:AAA36166.1; PID:g307116

R/Grundmann, U.; Abel, K.J.; Bohm, H.; Loebmann, H.; Lottspeich, F.; Kuepper, H.

Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988

A/Title: Characterization of cDNA encoding human placental anticoagulant protein (PP4):

A/Reference number: A30206; PMID:88234495; PMID:2967495

A/Accession: A30206

A/Molecule type: mRNA

A/Residues: 1-320 <GRU>

A/Cross-references: GB:M19384; NID:g189614; PIDN:AA59545.1; PID:g189615

R/Kaplan, R.; Jaffe, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.

J. Biol. Chem. 263, 8037-8043, 1988

A/Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phospholipid

A/Reference number: A28076; PMID:8828020; PMID:2967291

A/Accession: A28076

A/Molecule type: mRNA

A/Residues: 1-320 <KAP>

A/Cross-references: GB:U03745; NID:g182111; PIDN:AA53386.1; PID:g182112

R/Maurer-Poggy, I.; Reutelingersperger, C.P.M.; Pieters, J.; Bodo, G.; Stratowa, C.; Haupt

Eur. J. Biochem. 174, 585-592, 1988

A/Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-dependent

A/Reference number: S01016; PMID:88271329; PMID:2455636

A/Accession: S01016

A/Molecule type: mRNA

A/Residues: 1-320 <MAU>

A/Cross-references: EMBL:X12454; NID:g37636; PIDN:CAA30965.1; PID:g37637

A/Note: part of this sequence was confirmed by protein sequencing

R/Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 8087-8092, 1987

A/Title: Primary structure of human placental anticoagulant protein.

A/Reference number: A29417; PMID:88163463; PMID:2964863

A/Accession: A29417

A/Content: amino-terminal acetylation

A/Accession: A29417

A/Molecule type: mRNA

A/Residues: 1-320 <FUN>

A/Cross-references: EMBL:M18366; NID:g179131; PIDN:AAA35570.1; PID:g179132

R/Twaeski, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saito, Y.; Arai, K.; Mizoguchi, T.; Sato

J. Biochem. 102, 1261-1273, 1987

A/Title: Structure and expression of cDNA for an inhibitor of blood coagulation isolated

A/Reference number: A41514; PMID:88139278; PMID:2963810

A/Accession: A41514

A/Molecule type: mRNA

A/Residues: 1-320 <TWA>

A/Cross-references: GB:D00172; NID:g219480; PIDN:BA00122.1; PID:g219481

A/Note: part of this sequence was confirmed by protein sequencing

R/Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Haigler, H.T.

Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6083, 1987

A/Title: Structural and functional characterization of endonexin II, a calcium- and phos

A/Reference number: A28038; PMID:87317558; PMID:2957692

A/Accession: A28038

A/Molecule type: protein

A/Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>

R/Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.

J. Biol. Chem. 263, 18657-18663, 1988

A/Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2

inhibitor.

A/Reference number: A29696; PMID:89066652; PMID:2974032

A/Accession: C31953

A/Molecule type: protein

A/Residues: 85-93 <AHN>

R/Rochhut, B.; Comera, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Co

Biochem. J. 263, 929-935, 1989

A/Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with c

A/Reference number: S06646; PMID:90088443; PMID:12532007

A/Accession: S06646

A/Molecule type: protein

A/Residues: 7-25; 27-42; 51-74, 'X', 76-151; 181-198; 202-207; 209-226; 228-238; 246-271; 277-282,

R/Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.

FEBS Lett. 275, 15-21, 1990

A/Title: The calcium binding sites in human annexin V by crystal structure analysis at 2

A/Reference number: A37250; PMID:91085549; PMID:2148156

A/Accession: A37250

A/Content: annotation: X-ray crystallography, 2.0 angstroms

A/Note: three calcium ions are strongly bound at sites in the first, second, and fourth

R/Funakoshi, T.; Heitark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 5572-5578, 1987

A/Title: Human placental anticoagulant protein: isolation and characterization.

A/Reference number: A29670; PMID:88050845; PMID:2960376

A/Accession: A29670

A/Molecule type: protein

A/Residues: 29-73; 274-297; 300-320 <FU2>

R/Fernandez, M.P.; Morgan, R.O.; Fernandez, M.R.; Carcedo, M.T.

Gene 149, 253-260, 1994

A/Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C cont

A/Reference number: 137172; PMID:95047484; PMID:7958998

A/Accession: 137172

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-320 <RES>

A/Cross-references: EMBL:U01691; NID:g430964; PIDN:AA840047.1; PID:g430966

C/Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula

olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende

d clotting.

A/Genetic: GDB:ANX5

A/Cross-references: GDB:120555; OMIM:131230

A/Map position: 4q26-4q28

A/Supernotes: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3

C/Supernotes: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3

A/Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin

F:2-320/Product: annexin V #status experimental <MAT>

F:18-89/Domain: annexin repeat homology <AX1>

F:29-45/Region: endonexin fold #status predicted

F:90-161/Domain: annexin repeat homology <AX2>

F:101-117/Region: endonexin fold #status predicted

F:173-245/Domain: annexin repeat homology <AX3>

F:185-201/Region: endonexin fold #status predicted

F:249-320/Domain: annexin repeat homology <AX4>

F:260-276/Region: endonexin fold #status predicted

F:/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:/Binding site: phosphate (Thr) (covalent) #status predicted

F:28-30-32-72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experime

F:33-35-36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental

F:73-78/Binding site: calcium, low affinity (Leu, Glu) #status experimental

F:100-102-104-144/Binding site: calcium, high affinity (Leu, Gly, Asp) #status expe

F:259-261-263-303/Binding site: calcium, high affinity (Met, Gly, Asp) #status expe

Query Match 100.0% Score 1600; DB 1; Length 320;

Best Local Similarity 100.0%; Pred. No. 3-7e-96;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOVLRGTVTFPGFDERADAETLRKANKGCTDEESITLTLTSRSMOROBISAFTKL 60

DB 1 MAQVLRGTVTFPGFDERADAETLRKANKGCTDEESITLTLTSRSMOROBISAFTKL 60

QY 61 FGRDLDDKSELTKGFEKTLVAMKPSRLYDAVELKALKGAGTNERKVLTEIISRTPE 120

DB 61 FGRDLDDKSELTKGFEKTLVAMKPSRLYDAVELKALKGAGTNERKVLTEIISRTPE 120

QY 121 ELRAIKQVYEEBYGSSLEDVVGDTSGYGRMLVLLQANRDPAGIDAEQVEDPAQALF 180

Db 121 ELRAIKQVVEEYSSLEDVVDGTSYGRMLVLLQANRPDPAGIDEQVEDQALF 180
QY 181 QAGELKMGTEBEKFTITFGTSVSHLRKVPKWTISGFOIETIDETSQNLLEQALLAV 240
Db 181 QAGELKMGTEBEKFTITFGTSVSHLRKVPKWTISGFOIETIDETSQNLLEQALLAV 240
QY 241 VKSIRSIPTAYLAETLYYAMKAGAGTDDHTLIRVMSRSEIDLFNIRKERRKNFATSLYSMI 300
Db 241 VKSIRSIPTAYLAETLYYAMKAGAGTDDHTLIRVMSRSEIDLFNIRKERRKNFATSLYSMI 300
QY 301 KGDTSGDYKKALLLLCGEDD 320
Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 2

S27214
anexin V - bovine
N:Alternate names: CABP3; CABP7
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C:Accession: S27214; S27215
R:Leamouth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Giambanco, I.; Bi
Biochim. Biophys. Acta 1160, 76-83, 1992
A:Title: Novel isoforms of CABP 33/37 (Anexin V) from mammalian brain: structural and F
A:Reference number: S27214; MUID:93041974; PMID:1420335
A:Accession: S27214
A:Molecule type: protein
A:Residues: 1-320 <LEA>
A:Accession: S27215
A:Molecule type: protein
A:Residues: 1-35, 'T', '37-124', 'E', '126-320' <LE2>
A:Note: It is uncertain whether the sequence differences are due to allelic variation or
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
Olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
F:17-88/Domain: annexin repeat homology <AX1>
F:128-44/Region: endonexin fold #status predicted
F:189-160/Domain: endonexin repeat homology <AX2>
F:100-116/Region: endonexin repeat homology <AX3>
F:172-244/Domain: annexin repeat homology <AX4>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:22/Binding site: phosphate (Thr) (covalent) #status experimental
F:27,29,31,71/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicte
F:32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F:72,77/Binding site: calcium, low affinity (Leu, Gly, Asp) #status predicte
F:99,101,103,143/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predi
F:258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status predi

Query Match 96.6%; Score 1545.5; DB 1; Length 320;
Best Local Similarity 96.9%; Pred. No. 1.2e-92;
Matches 310; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 2 AOVLRGTVDPFGPDERADAEFLRKAMKGLCTDEBSITLTLTSNSNORQISAAFTLFG 61
Db 1 AOVLRGTVADPFGPDERADAEFLRKAMKGLCTDEBSITLTLTSNSNORQISAAFTLFG 60
QY 62 GRDLIDDLKSELTKGFEKLYALMKPSRLVAYELKHALKGAGTNEKVLTEIIASRTPEE 121
Db 61 GRDLIDDLKSELTKGFEKLYALMKPSRLVAYELKHALKGAGTNEKVLTEIIASRTPEE 120
QY 122 LRATKQVVEEYSSLEDVVDGTSYGRMLVLLQANRPDPAGIDEQVEDQALFQ 181
Db 121 LRATKQVVEEYSSLEDVVDGTSYGRMLVLLQANRPDPAGIDEQVEDQALFQ 180
QY 182 AGELKMGTEBEKFTITFGTSVSHLRKVPKWTISGFOIETIDETSQNLLEQALLAV 241

Db 181 AGELKMGTEBEKFTITFGTSVSHLRKVPKWTISGFOIETIDETSQNLLEQALLAV
QY 242 KSIIRSIPTAYLAETLYYAMKAGAGTDDHTLIRVMSRSEIDLFNIRKERRKNFATSLYSMI
Db 241 KSIIRSIPTAYLAETLYYAMKAGAGTDDHTLIRVMSRSEIDLFNIRKERRKNFATSLYSMI
QY 302 KGDTSGDYKKALLLLCGEDD 320
Db 301 KGDTSGDYKKALLLLCGEDD 320

RESULT 3

LUR15
anexin V - rat
N:Alternate names: endonexin II; lipocortin V; placental
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-19
C:Accession: C29250; S66680
R:Peppinsky, R.B.; Tizard, R.; Matallano, R.J.; Sinclair, L.K.; Miller, G
J. Biol. Chem. 263, 10799-10811, 1988
A:Title: Five distinct calcium and phospholipid binding proteins share ho
A:Reference number: A92659; MUID:88273202; PMID:2968983
A:Accession: C29250
A:Molecule type: mRNA
A:Residues: 1-319 <PEP>
A:Cross-references: GB:M21730; NID:G205138; PID:AAA41512.1; PID:G205139
R:Imai, Y.; Kohnaka, S.
Eur. J. Biochem. 232, 327-334, 1995
A:Title: Structure of rat annexin V gene and molecular diversity of its t
A:Reference number: S66680; MUID:96035863; PMID:7556178
A:Accession: S66680
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <IMA>
A:Cross-references: EMBL:D42136
C:Comment: Annexin V has been proposed to play a role in the inhibition of
Olipid-binding rather than proteolytic inactivation. It does not affect t
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; duplication; endonexin fold; membrane-associ
F:2-319/Product: annexin V #status predicted <MAT>
F:16-87/Domain: annexin repeat homology <AX1>
F:27-43/Region: endonexin fold #status predicted
F:88-159/Domain: annexin repeat homology <AX2>
F:99-115/Region: endonexin repeat homology <AX3>
F:171-243/Domain: annexin repeat homology <AX4>
F:183-199/Region: endonexin fold #status predicted
F:247-318/Domain: annexin repeat homology <AX4>
F:258-274/Region: endonexin fold #status predicted
F:26,28,30,70/Binding site: calcium, high affinity (Met, Gly, Gly, Glu)
F:32,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status p
F:71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F:98,100,102,142/Binding site: calcium, high affinity (Leu, Gly, Gly, As
F:257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, A

Query Match 91.5%; Score 1464.5; DB 1; Length 319;
Best Local Similarity 92.4%; Pred. No. 2e-87;
Matches 292; Conservative 12; Mismatches 12; Indels 1; Gap

QY 5 LRGVTVDPFGPDERADAEFLRKAMKGLCTDEBSITLTLTSNSNORQISAAFTLFG
Db 3 LRGVTVDPFGPDERADAEFLRKAMKGLCTDEBSITLTLTSNSNORQISAAFTLFG
QY 65 LRDLIDDLKSELTKGFEKLYALMKPSRLVAYELKHALKGAGTNEKVLTEIIASRTPEE
Db 63 LRDLIDDLKSELTKGFEKLYALMKPSRLVAYELKHALKGAGTNEKVLTEIIASRTPEE
QY 125 IKQVVEEYSSLEDVVDGTSYGRMLVLLQANRPDPAGIDEQVEDQALFQ

Db 123 IKQAVEEYSGNLEDDVVDTSYGYQRMVLVLLQANRPDPAIDAQVELDAQALFQAGE 182

Qy 185 LKMGDEEFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRENSGNLEQLLAVVSI 244

Db 183 LKMGDEEFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRENSGNLEQLLAVVSI 242

Qy 245 RSPAYLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNATSLYSMIKDT 304

Db 243 RSPAYLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNATSLYSMIKDT 302

Qy 305 SGDYKALLLC-GEED 320

Db 303 SGDYKALLLC-GEED 319

RESULT 4

LUCIS

annexin V - chicken

N/Alternate names: anchoring CII; endonexin II; lipocortin V; placental anticoagulant pro

C/Species: Gallus gallus (chicken)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 02-Jun-2000

C/Accession: A35381; A28623; B40404; S32523; S08771

R/Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfeaffle, M.; Deutzmann, R.; Mc

J. Biol. Chem. 265, 8344, 1990

A/Reference number: A35381; MUID:90243721; PMID:2159478

A/Contents: extractum

A/Accession: A35381

A/Molecule type: mRNA

A/Residues: 1-321 <PER>

A/Cross-references: GB:M30971; GB:J03194; NID:G211138; PIDN:AAA8591.1; PID:G211139

R/Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfeaffle, M.; Deutzmann, R.; Mc

J. Biol. Chem. 263, 5921-5925, 1988

A/Title: The structure of anchoring CII, a collagen binding protein isolated from chondro

A/Reference number: A28623; MUID:8816921; PMID:2833522

A/Accession: A28623

A/Molecule type: mRNA

A/Residues: 1-118; LKICILIRFNMQYEANLGRNKITGRHQAIFRDQWSSCRQIEI', 163-167, 'R', 169-321 <

R/Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.

J. Biol. Chem. 266, 10678-10685, 1991

A/Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective particl

A/Reference number: A40404; MUID:91244852; PMID:2037607

A/Accession: B40404

A/Molecule type: protein

A/Residues: 188-199 <GEN>

A/Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched micros

R/Boutead, C.M.; Brown, R.; Walker, J.H.

Biochem. J. 291, 601-608, 1993

A/Title: Isolation, characterization and localization of annexin V from chicken liver.

A/Reference number: S32523; MUID:93249384; PMID:8484740

A/Accession: S32523

A/Status: preliminary

A/Molecule type: protein

A/Residues: 6-20,85,'X',87-88,'X',90-93,'X',95-96,'XX',99-100,'X',102-103,'XX',106-107;1

C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

deroscod.

C/Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula

olipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende

C/Keywords: calcium binding; collagen binding; duplication; endonexin fold; membrane-ass

F/2-321/Product: annexin V #status predicted <MNT>

F/18-89/Domains: annexin repeat homology <AX1>

F/29-45/Region: endonexin fold #status predicted

F/101-161/Domains: annexin repeat homology <AX2>

F/101-117/Region: endonexin fold #status predicted

F/173-245/Domains: annexin repeat homology <AX3>

F/185-201/Region: endonexin fold #status predicted

F/249-320/Domains: annexin repeat homology <AX4>

F/260-276/Region: endonexin fold #status predicted

F/28-30,32,72/Binding site: calcium, high affinity (Met, Gly, Gln) #status predicted

F/33,35,36/Binding site: calcium, low affinity (Ileu, Gln) #status predicted

F/73,78/Binding site: calcium, low affinity (Ileu, Gln) #status predicted

F/100,102,104,144/Binding site: calcium, high affinity (Ile, Gly, Gln) #status pred

F/259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gln, Asp) #status pre

Query Match 80.6%; Score 1289; DB 1; Length 321;

Best Local Similarity 78.4%; Pred. No. 4,36-76;

Matches 251; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MAQVLRRTVDFPSPEDRAAETLRKAMKIGTDEESITLTLRSNAQOETSAARFTL 60

Db 1 MAKYRTGVAFSPSPEDRAAETLRKAMKIGTDEESITLTLRSNAQOETSAARFTL 60

Qy 61 FGRDLDDLSLTKGKEXLIVALKMPSRLYDAVELKHAIGKGTNKKLTETIASTPE 120

Db 61 FGRDLVDDLSLTKGKEXLIVALKMPSRLYDAVELKHAIGKGTNKKLTETIASTPE 120

Qy 121 ELRAIKQVEEYSGSLEDDVVDTSYGYQRMVLVLLQANRPDPAIDAQVELDAQALF 180

Db 121 EVGNIKQVWQYVEANEDKITGETSGHFRLLVLLQANRPDPAIDAQVELDAQALF 180

Qy 181 QAGELKMGDEEFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRENSGNLEQLLAV 240

Db 181 RAGELKMGDEEFTITFGTRSVSHLRKVPDKYMTISGFOIETTIDRENSGNLEQLLAV 240

Qy 241 VKSIRSPAYLAETLYYAMKAGAGTDHTLIRVWVSSEIDLFNIRKEFRKNATSLYSMT 300

Db 241 VKCIRSPAYLAETLYYAMKAGAGTDHTLIRVWVSSEIDLIRHFRKNATSLYSMT 300

Qy 301 KQDTSQDYKALLLC-GEED 320

Db 301 QKQTSQDYKALLLC-GEED 320

RESULT 5

annexin VI - mouse

N/Alternate names: calcium-binding protein p68; calelectrin; calphobindin II

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1989 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: S01786

R/Moss, S.E.; Crumpton, M.R.; Crumpton, M.J.

Eur. J. Biochem. 177, 21-27, 1988

A/Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family

A/Reference number: S01786; MUID:89030687; PMID:2972541

A/Accession: S01786

A/Molecule type: mRNA

A/Residues: 1-673 <MOS>

A/Cross-references: EMBL:X13460; NID:953580; PIDN:CAA31808.1; PID:953581

A/Note: the authors translated the codon GGC for residue 329 as Gly

C/Comment: This abundant cytosolic protein binds to the inner surface of the cell membra

C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol

F/2-673/Product: annexin VI #status predicted <MNT>

F/2-673/Domains: annexin repeat homology <AX1>

F/34-50/Region: endonexin fold #status predicted

F/195-166/Domains: annexin repeat homology <AX2>

F/106-122/Region: endonexin fold #status predicted

F/178-250/Domains: annexin repeat homology <AX3>

F/190-206/Region: endonexin fold #status predicted

F/254-325/Domains: annexin repeat homology <AX4>

F/265-281/Region: endonexin repeat homology <AX5>

F/366-437/Domains: annexin repeat homology <AX6>

F/377-393/Region: endonexin fold #status predicted

F/438-509/Domains: annexin repeat homology <AX6>

F/449-466/Region: endonexin fold #status predicted

F/527-596/Domains: annexin repeat homology <AX7>

F/538-554/Region: endonexin fold #status predicted

F/602-673/Domains: annexin repeat homology <AX8>

F/613-629/Region: endonexin fold #status predicted

F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.9%; Score 942; DB 1; Length 673;

Best Local Similarity 59.4%; Pred. No. 2,76-53;

Matches 187; Conservative 49; Mismatches 79; Indels 0; Gaps 0;

	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
Qy	7	58.3%; Score 933; DB 1; Length 321;	58.6%; Pred. No. 4.1e-53;	53;	77;	0;	0;
Db	8	58.3%; Score 933; DB 1; Length 321;	58.6%; Pred. No. 4.1e-53;	53;	77;	0;	0;
Qy	67	58.3%; Score 933; DB 1; Length 321;	58.6%; Pred. No. 4.1e-53;	53;	77;	0;	0;

1117 **business**

[illegible]

Query Match 58.2%; Score 931; DB 1; Length 318;
 Best Local Similarity 58.9%; Pred. No. 5.4e-53;
 Matches 185; Conservative 51; Mismatches 78; Indels 0; Gaps 0;

QY 7 GTVDFPFGEDRAAEATLRKAMKGLGTHDEEILTLTSSRAQOEISAAKTLFGDRL 66
 DB 5 GTVAAAGGFAAEADQTLRKAMKGLGTHDEDAIISVLAIRSTAOROEIRTAVKSTIGDRL 64
 QY 67 DDLKSELTKPEKELIYALMKPSRLYDAVELKHALKGAGTNKVLTEIATSPPELAAIK 126
 DB 65 DDLKSELTKPEKELIYALMKPSRLYDAVELKHALKGAGTNKVLTEIATSPPELAAIK 124
 QY 127 QVVEEYGGSLIEDVDVDTSGYGYORMLVLLQANRPDAGIDEAQVEODQALFOAGELK 186
 DB 125 QVYQLAQGRSLEDIDRSDFSMFORVLVLSAGRDENYIDDLVYQDQOLYEAGSKK 184
 QY 187 WGTDEEFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAAVKSIRS 246
 DB 185 WGTDEVKFLTVLCSRNNHLLHVFDEYKRISQKQIEGSIKSEISGSPEDALALVKCMRN 244
 QY 247 IIPVLAETLYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPFATSLYMIKGDTS 306
 DB 245 KSAIFAEFLYKSMKGLGTDNTLIRVWVSRAEIDMDIRANFKRLYKSLYSFKDTS 304
 QY 307 DYKALLLLCGEDD 320
 DB 305 DYKALLLLCGEDD 318

RESULT 8

S52844

annexin VI - rat

N/Alternate names: calcium-binding protein 65/67

C/Species: Rattus norvegicus (Norway rat)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S65683; S52844

R/Fan, H.; Jösic, D.; Lim, Y.P.; Reutter, W.

Eur. J. Biochem. 230, 741-751, 1995

A/Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-binding

A/Reference number: S65683; MUID:9531313; PMID:7607247

A/Accession: S65683

A/Molecule type: mRNA

A/Residues: 1-673 <PAN>

A/Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181

A/Experimental source: liver

C/Suprafamily: annexin VI; annexin repeat homology

C/Keywords: acetylated amino end; calcium binding; endonexin fold; membrane-associated p

F/2-673/Product: annexin VI #status predicted <MAT>

F/23-94/Domain: annexin repeat homology <AX1>

F/34-50/Region: endonexin fold #status predicted

F/95-166/Domain: annexin repeat homology <AX2>

F/106-122/Region: endonexin fold #status predicted

F/178-250/Domain: annexin repeat homology <AX3>

F/190-206/Region: endonexin fold #status predicted

F/254-325/Domain: annexin repeat homology <AX4>

F/365-281/Region: endonexin fold #status predicted

F/365-437/Domain: annexin repeat homology <AX5>

F/377-393/Region: endonexin repeat homology <AX6>

F/438-509/Domain: annexin repeat homology <AX6>

F/449-465/Region: endonexin fold #status predicted

F/527-598/Domain: annexin repeat homology <AX7>

F/538-554/Region: endonexin fold #status predicted

F/602-673/Domain: annexin repeat homology <AX8>

F/613-629/Region: endonexin fold #status predicted

F/2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.2%; Score 931; DB 1; Length 673;
 Best Local Similarity 59.0%; Pred. No. 1.4e-52;
 Matches 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;

QY 6 RGTVDFFGPFERDAETLRKAMKGLGTHDEEILTLTSSRAQOEISAAKTLFGDRL 65
 DB 186; Conservative 48; Mismatches 81; Indels 0; Gaps 0;

DB 11 RGSVHDEADPDANDADALYAMKFGSDKESILELITSSNNKQOEICQSYSLYKGLD 70
 QY 66 LDDKSELTKPEKELIYALMKPSRLYDAVELKHALKGAGTNKVLTEIATSPPELAAIK 125
 DB 71 IADLYELTKPEKELIYALMKPSRLYDAVELKHALKGAGTNKVLTEIATSPPELAAIK 120
 QY 126 QVVEEYGGSLIEDVDVDTSGYGYORMLVLLQANRPDAGIDEAQVEODQALFOAGELK 185
 DB 131 VAAKVAEYDLSDDIIGDTSQHFKQLVLLQGTENDDVSEDLVQDQOLYEAGEL 190
 QY 186 WGTDEEFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAAVKSIRS 245
 DB 191 WGTDEEFTITFGTRSVSHLRKVPDKYMTISGFOIEETIDRETSGNLEQLLAAVKSIRS 240
 QY 246 SIPIVLAETLYAMKAGTDDHTLIRVWVSRSSEIDLFNIRKFRKPFATSLYMIKGDTS 305
 DB 251 STPEYFAERLFRKAMKGLGTDNTLIRVWVSRAEIDMDIRANFKRLYKSLYSFKDTS 310
 QY 306 GDYKALLLLCGEDD 320
 DB 311 GEYKALLLLCGEDD 325

RESULT 9

A0H068

annexin VI [validated] - human

N/Alternate names: calcium-binding protein, 68k; calelectrin; calphobindin II

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000

C/Accession: J00032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507

R/Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; Sh

J. Biochem. 106, 43-49, 1989

A/Title: Structure and expression of cDNA for calphobindin II, a human placental coagula

A/Reference number: J00032; MUID:89380132; PMID:2528541

A/Accession: J00032

A/Molecule type: mRNA

A/Residues: 1-673 <IMA>

A/Cross-references: EMBL:D00510; NID:g219550; PIDN:BA00400.1; PID:g219551

R/Crompton, M.R.; Owens, R.J.; Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crompton, M.J.

EMBO J. 7, 21-27, 1988

A/Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68:

A/Reference number: S00263; MUID:88196081; PMID:3258820

A/Accession: S00263

A/Molecule type: mRNA

A/Residues: 1-618; 'D', 620-673 <CR1>

A/Cross-references: EMBL:Y00097; NID:g35217; PIDN:CAA68286.1; PID:g35218

A/Accession: S18519

A/Molecule type: protein

A/Residues: 103-113; 167-172, 'X', 174-177; 232-235, 'F', 237-240; 251-258; 277-281; 359-362, 'G',

A/Note: The sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu

R/Suehof, T.C.; Slaughter, C.A.; Leznicki, I.; Barton, P.; Reynolds, G.A.

Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988

A/Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-kDa

A/Reference number: A31079; MUID:88124902; PMID:2963335

A/Accession: A31079

A/Molecule type: mRNA

A/Residues: 1-225, 'MK', 228-554, 'T', 556-673 <SUB>

A/Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g179976

R/Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shitarauchi, M.; Shidara, Y.; Maki, M.

J. Biochem. 107, 43-50, 1990

A/Title: Structure and properties of calphobindin II, an anticoagulant protein from huma

A/Reference number: JX0091; MUID:90236978; PMID:2139657

A/Accession: JX0091

A/Molecule type: protein

A/Residues: 2-299; 307-314; 320-445; 447-549; 581-673 <YOS>

R/Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.

J. Biol. Chem. 264, 17222-17230, 1989

A/Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding protein

A/Reference number: A34459; MUID:9008880; PMID:2529258

A/Accession: B34459

A/Molecule type: protein

A/Residues: 10-25; 69-75; 136-151; 192-207; 209-220; 300-306 <HAY>

A:Experimental source: placenta
R.Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2
inhibitor.
A:Reference number: A92696; MUID:89066652; PMID:2974032

A:Accession: B31953

A:Molecule type: protein
A:Residues: 90-108, 'L', 110-126, 127, 265-276, 286-302, 626-654 <AHN>

R:Hyatt, S.U.; Liao, L.; Chapline, C.; Jaken, S.
Biochemistry 33, 1223-1228, 1994

A:Title: Identification and characterization of alpha-protein kinase C binding proteins
A:Reference number: A53507; MUID:94153907; PMID:8110754

A:Accession: A53507

A:Molecule type: protein
A:Residues: 'X', 473-480, 'DY' <HYA>

C:Comment: This abundant cytosolic protein binds to the inner surface of the cell membrane

C:Genetics:

A:Gene: GDB:ANK6
A:Cross-references: GDB:119681; OMIM:114070

A:Map position: 5q32-5q34
C:Superfamily: annexin VI; annexin repeat homology

C:Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol
F:2-673/Product: annexin VI #status experimental <MAT>

F:23-94/Domain: annexin repeat homology <AX1>
F:34-50/Region: endonexin fold #status predicted

F:95-166/Domain: annexin repeat homology <AX2>
F:106-122/Region: endonexin fold #status predicted

F:178-250/Domain: annexin repeat homology <AX3>
F:190-206/Region: endonexin fold #status predicted

F:254-325/Domain: annexin repeat homology <AX4>
F:365-481/Region: endonexin fold #status predicted

F:565-637/Domain: annexin repeat homology <AX5>
F:777-933/Region: endonexin fold #status predicted

F:348-509/Domain: annexin repeat homology <AX6>
F:449-465/Region: endonexin fold #status predicted

F:527-598/Domain: annexin repeat homology <AX7>
F:538-554/Region: endonexin fold #status predicted

F:602-673/Domain: annexin repeat homology <AX8>
F:613-629/Region: endonexin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (1n mature form) #status experimental

Query Match 57.8%; Score 927; DB 1; Length 673;

Best Local Similarity 57.8%; Pred. No. 2.5e-52;

Matches 182; Conservative 52; Mismatches 81; Indels 0; Gaps 0;

6 RGTWDPFGPDERADAEITLRKAMKGLGTDSESIITLTLRSNAQROEISAFAKTLFGRLD 65

11 RGSIHDPFGDPNDADALVYAMKFGSDKEALIDITSRNROREVCOSKSLYKDL 70

66 LDDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPEELRAI 125

71 IADLKVELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPEELRAI 130

126 KQVEEYGGSLDDVDVDTSGYQRMVLTLLQNRDPDAGIDEAQNVEDQALFOAGEL 185

131 VAAKYDAVERDLDDIDITSGHFQKMLVLLQGTREDDVASELVQDDVQDLYAEEL 190

186 KMGTDSEKTIITFGRRSHLRKVDKMTISGFOIEETIDETSNGLEQLLAVKSIK 245

191 KMGTDSEKTIITFGRRSHLRKVDKMTISGFOIEETIDETSNGLEQLLAVKSIK 250

246 SIPVLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFIKREFRKNFATSLYSMTKGDTS 305

251 STPEYFAERLFRAMKGLGTRDNTLIRVWVSRSSEIDLFIKREFRKNFATSLYSMTKGDTS 310

306 GDYKKAALLLCGEDD 320

311 GEYKKTLLKLSGGDD 325

RESULT 10

LUBO4

annexin IV - bovine

N:Alternate names: 33k calelectrin; chromobindin IV; endonexin; lipocortin

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1992 #sequence revision 10-Sep-1992 #text change 22-Jun-19

C:Accession: A1578; D45066; S59624; A45066; B45066; C45066; G45066; H45066; I45066; J45066; K45066; L45066; M45066; N45066; O45066; P45066; Q45066; R45066; S45066; T45066; U45066; V45066; W45066; X45066; Y45066; Z45066

R:Hamman, H.C.; Gaffey, L.C.; Lynch, K.R.; Creutz, C.E.
Biochem. Biophys. Res. Commun. 156, 660-667, 1988

A:Title: Cloning and characterization of a cDNA encoding bovine endonexin

A:Reference number: A1578; MUID:89050088; PMID:2847715

A:Accession: A1578

A:Molecule type: mRNA

A:Residues: 1-119 <HAM>

A:Cross-references: GB:X13627; NID:9245; PIDN:CA31954.1; PID:9246; GB:M2

J. Biol. Chem. 267, 20336-20339, 1992

A:Title: Carbohydrate-binding proteins in bovine kidney have consensus am

A:Reference number: A45066; MUID:93015942; PMID:1400371

A:Accession: D45066

A:Molecule type: protein

A:Residues: 10-18, 'X', 20-22, 'X', 24-25, 29-48, 101-107, 'X', 109-118, 'X', 194-1

A:Experimental source: kidney

A:Note: sequence extracted from NCBI backbone (NCBIP:116211, NCBIP:116206

A:Note: these fragments are derived from a 33k protein that exhibited Ca-

R:Solma, H.; Matsushima, N.; Watanabe, T.; Hattori, A.; Kuroki, Y.; Akino

Biochem. J. 312, 175-181, 1995

A:Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A

A:Reference number: S59624; MUID:96077142; PMID:7492310

A:Accession: S59624

A:Status: preliminary

A:Molecule type: protein

A:Residues: 29-44; 72-77; 112-119; 163-180; 181-190; 226-235 <SOH>

C:Comment: Annexins undergo reversible, calcium-dependent binding to mem

C:Superfamily: annexin I; annexin repeat homology

C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein;

F:2-319/Product: annexin IV #status predicted <MAT>

F:17-88/Domain: annexin repeat homology <AX1>

F:28-44/Region: endonexin fold #status predicted

F:89-160/Domain: annexin repeat homology <AX2>

F:100-116/Region: endonexin fold #status predicted

F:112-244/Domain: annexin repeat homology <AX3>

F:184-200/Region: endonexin fold #status predicted

F:248-319/Domain: annexin repeat homology <AX4>

F:259-275/Region: endonexin fold #status predicted

F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #stat

F:155,245/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.8%; Score 924; DB 1; Length 319;

Best Local Similarity 58.3%; Pred. No. 1.5e-52;

Matches 183; Conservative 51; Mismatches 80; Indels 0; Gaps 0;

7 GTVWDPFGPDERADAEITLRKAMKGLGTDSESIITLTLRSNAQROEISAFAKTLFGRLD 65

6 GTVWDPFGPDERADAEITLRKAMKGLGTDSESIITLTLRSNAQROEISAFAKTLFGRLD 70

66 DDLKSELTGKFEKLIYALMKPSRLYDAVELKHALKGAGTNEKVLTEIARTPEELRAI 125

127 KQVEEYGGSLDDVDVDTSGYQRMVLTLLQNRDPDAGIDEAQNVEDQALFOAGEL 185

126 QTYLQYGRSLDDVIRSDTSGFQKMLVLLQGTREDDVASELVQDDVQDLYAEEL 190

187 KMGTDSEKTIITFGRRSHLRKVDKMTISGFOIEETIDETSNGLEQLLAVKSIK 245

186 KMGTDSEKTIITFGRRSHLRKVDKMTISGFOIEETIDETSNGLEQLLAVKSIK 250

247 IPVLAETLYYAMKAGTDDHTLIRVWVSRSSEIDLFIKREFRKNFATSLYSMTKGDTS 305

246 KSAVFAERLFRAMKGLGTRDNTLIRVWVSRSSEIDLFIKREFRKNFATSLYSMTKGDTS 310

307 DYKKAALLLCGEDD 320

311 GEYKKTLLKLSGGDD 325

RESULT 10

LUBO4

Db 306 DYKVLTLICGGDD 319

RESULT 11

JC2029

annexin - chicken

N/Alternate names: gallus lipid-dependent Ca²⁺-binding protein

C/Species: Gallus gallus (chicken)

C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

C/Accession: JC2029

R/Towle, X.; Genge, B.R.; Wu, L.N.Y.; Buzzzi, W.R.; Showman, R.M.; Wuthier, R.E.

Biochem. Biophys. Res. Commun. 197, 556-561, 1993

A/Title: Characterization, cloning and expression of the 67-kDa annexin from chicken giv

A/Reference number: JC2029; MUID:94092130; PMID:8267590

A/Accession: JC2029

A/Molecule type: mRNA

A/Residues: 1-671 <CAO>

C/Superfamily: annexin VI; annexin repeat homology

C/Keywords: calcium binding; phospholipid binding

F/21-92/Domain: annexin repeat homology <AX1>

F/93-164/Domain: annexin repeat homology <AX2>

F/176-248/Domain: annexin repeat homology <AX3>

F/252-323/Domain: annexin repeat homology <AX4>

F/364-435/Domain: annexin repeat homology <AX5>

F/436-507/Domain: annexin repeat homology <AX6>

F/525-597/Domain: annexin repeat homology <AX7>

F/601-671/Domain: annexin repeat homology <AX8>

Query Match 56.5%; Score 904.5; DB 2; Length 671;

Best Local Similarity 58.0%; Pred. No. 6.9e-51;

Matches 165; Conservative 51; Mismatches 82; Indels 1; Gaps 1;

```

3 QVLRGVTFDPGDERADAEITLRKAMKGLGTDEESITLTLSRSNAQROEISAAPKTLRG 62
6 KYVRGSKVDPGPNASQDADALCNAMKRGSDKDALDLTSSNQREITCOAVSYQSG 65
63 RLILDLKSELGKFEKLIVALKMPSRLYDAVELKHALKGATNEKYLTEIYASRPEEL 122
66 KDLIDLKTELTGKFERLIYSLMRPPAYSAKEIKHALIGIDKCLIEIILASRINQET 125
123 RLKQVVEEYSSLEDDVVGDTSGYQRMVLLQANRDPAGIDEAQUEQDAQALFOA 182
126 HDLVAAVYKQAYERDEADVVGDTSGHFKMVLVLLQGAEEEDVVEEDLEQDAKOLLEA 185
183 GELKMGTEDEKFTTIGTRSVSHTLRKVPDKYMTISGFOIEETIDRTSGNLEQLIAVVK 242
186 GELKMGTEDEKFTTIGTRSVSHTLRKVPDKYMTISGFOIEETIDRTSGNLEQLIAVVK 245
243 SIRSIPAYLAETLYAMKAGTDDHTLIRVWVSRSRIDEFNIRKFRKRFATSLYSMTKG 302
246 CVRSIAEYFAEKLTYAMKAGTDDHTLIRVWVSRSRIDEFNIRKFRKRFATSLYSMTKG 305
303 DTSGDYKALLLLC-GEED 320
306 DTSGDYKALLLLC-GEED 324

```

RESULT 12

LUBO11

annexin XI form A - bovine

N/Alternate names: calyculin-associated protein peptide, CAP-50

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C/Accession: A42113; MUID:92184796; PMID:1372001

R/Towle, C.A.; Treadwell, B.V.

J. Biol. Chem. 267, 5416-5423, 1992

A/Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis, a

A/Reference number: A42113; MUID:92184796; PMID:1372001

A/Accession: A42113

A/Molecule type: mRNA

A/Residues: 1-503 <TOM>

A/Cross-References: GB:M82802; NID:G162673; PIDN:AAA0379.1; PID:G162674

A/Note: the authors did not translate the codon GAC for residue 503

R/Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka, T. Biol. Chem. 267, 13498-13504, 1992

A/Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast

A/Reference number: A42909; MUID:92317074; PMID:1618851

A/Accession: A42909

A/Molecule type: Protein

A/Residues: 213-223, 'X', 225-226, 319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339, 441-450, 'X',

A/Experimental source: lung

A/Note: sequence modified after extraction from NCBI backbone

C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

derol.

C/Genetics:

A/Introns: 19/1; 56/2

A/Note: the list of introns is incomplete

C/Superfamily: annexin VII; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F/201-272/Domain: annexin repeat homology <AX1>

F/212-228/Domain: endonexin fold #status predicted

F/273-344/Domain: annexin repeat homology <AX2>

F/284-300/Region: endonexin fold #status predicted

F/356-428/Domain: annexin repeat homology <AX3>

F/368-384/Region: endonexin fold #status predicted

F/432-503/Domain: annexin repeat homology <AX4>

F/443-459/Region: endonexin fold #status predicted

F/59,111/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.7%; Score 875; DB 1; Length 503;

Best Local Similarity 55.2%; Pred. No. 3.9e-49;

Matches 174; Conservative 58; Mismatches 83; Indels 0; Gaps 0;

```

6 RGVTFDPGDERADAEITLRKAMKGLGTDEESITLTLSRSNAQROEISAAPKTLRG 65
189 RGVTFDPGDERADAEITLRKAMKGLGTDEESITLTLSRSNAQROEISAAPKTLRG 248
66 LDDLKSELGKFEKLIVALKMPSRLYDAVELKHALKGATNEKYLTEIYASRPEEL 125
249 IVDLSELGKFEKLIVALKMPSRLYDAVELKHALKGATNEKYLTEIYASRPEEL 308
126 KQVVEEYSSLEDDVVGDTSGYQRMVLLQANRDPAGIDEAQUEQDAQALFOA 185
309 NKVYTFEPKTLIEARISTSGHFORLLISQGRDESTNVDMTLVQDVELYAGGN 368
186 KMGTEDEKFTTIGTRSVSHTLRKVPDKYMTISGFOIEETIDRTSGNLEQLIAVVK 245
369 RLGTDESKFNALLCSRSRAHLVAVENEYQMTGRIDEKSGDLEQGLAVVCKLK 428
246 SIRSIPAYLAETLYAMKAGTDDHTLIRVWVSRSRIDEFNIRKFRKRFATSLYSMTKG 305
429 NTPAFEAERLWYAMKAGTDDHTLIRVWVSRSRIDEFNIRKFRKRFATSLYSMTKG 488
306 GPKYKALLLLC-GEED 320
489 GPKYKALLLLC-GEED 503

```

RESULT 13

S23447

annexin XI form B - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 22-Jun-1999

C/Accession: S23447; S36136

R/Towle, C.

submitted to the EMBL Data Library, February 1992

A/Reference number: S23447

A/Accession: S23447

A/Molecule type: mRNA

A/Residues: 1-505 <TOM>

A/Cross-References: EMBL:Z11742; NID:G77; PIDN:CAA77801.1; PID:G78

R/Towle, C.A.; Weisbach, L.; Treadwell, B.V.

Biochim. Biophys. Acta 1131, 223-226, 1992

A/Title: Alternatively spliced annexin XI transcripts encode proteins that differ near t

A/Reference number: S36136; MUID:92305067; PMID:1535225

A/Accession: S36136
 A/Molecule type: mRNA
 A/Residues: 1-77 <TO>
 A/Cross-references: EMBL:Z11742
 C/Comment: Annexins undergo reversible, calcium dependent binding to membrane phospholipid headgroup.
 C/Genetics:
 A/Introns: 19/1; 58/2
 A/Note: The list of introns is incomplete
 C/Superfamily: annexin VII; annexin repeat homology
 C/Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glycoprotein
 F/203-274/Domain: annexin repeat homology <AX1>
 F/214-223/Region: endonexin fold #status predicted
 F/214-223/Region: endonexin repeat homology <AX2>
 F/275-346/Domain: annexin repeat homology <AX3>
 F/286-302/Region: endonexin fold #status predicted
 F/358-430/Domain: annexin repeat homology <AX3>
 F/370-386/Region: endonexin fold #status predicted
 F/434-505/Domain: annexin repeat homology <AX4>
 F/445-461/Region: endonexin fold #status predicted
 F/611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.7%; Score 875; DB 1; Length 505;
 Best Local Similarity 55.2%; Pred. No. 3.9e-49;
 Matches 174; Conservative 58; Mismatches 83; Indels 0; Gaps 0;

QY 6 RGVTDPPGFDERADATLRKAMKGLGTDEESILTLTSSNAQOEISAFTLFGRL 65
 DB 191 RGTITDASGFDLRBAEVLKAMKGGTDEQAIIIDCGSRNKORQOILLSPFTAYGKDL 250
 QY 66 LDDKSELGTGFEKLIVALKPSRLYDAVELKALKGAGTNEKVLTEIASSRPEELR 125
 DB 251 IKDLKSELGNFEKTLTALMKTPVLPFAVEIKAIKAGDEACLEIILASSRNEHIR 310
 QY 126 KOYEEBEGSSLEDVVGTSYQRMVVLQANRDPAGIDEADEVDAQALFOAGEL 185
 DB 311 NRYYKTEFFKLTLEAARSDTSQHPQLLSLQGNBESNTVDMSLVQDVGELVYAG 370
 QY 126 KMGTDDEKFTITGTSVSHLRKVPKMTISGFOIETITDRSGNLQDLAVYKS 245
 DB 371 RLGTDESKFNAVLCSRRALHVAVFNEYQMTGDIKSIKREMSDGLQGLAVVCLK 430
 QY 246 SIPAVLAETLYYAMKAGTDDHTLIRVWSSRSEIDLFNIRKERRKPFATSLYSMIK 305
 DB 431 NTPAFPAERLNKMRGAGTDRTLIRIMVSRSEIDLDIRAERYRLVKGSLYHDITDTS 490

QY 306 GDYKALLLLCGEDD 320
 DB 491 GDYKILLKTCGND 505

RESULT 14
 LURB11
 N/Alternate names: calyculin-associated annexin protein CAP-50
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Jun-2000
 C/Accession: JH0694; PH0950; A38250; PS0263
 R/Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 186, 1227-1235, 1992
 A/Title: Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.
 A/Reference number: JH0694; MUID:92378579; PMID:1380798
 A/Accession: JH0694
 A/Molecule type: mRNA
 A/Residues: 1-503 <TO>
 A/Cross-references: DDBJ:D10883; NID:g471147; PIDN:BA01705.1; PID:g471148
 A/Experimental source: Lung
 A/Accession: PH0950
 A/Molecule type: protein
 A/Residues: 104-141;213-231;254-262;270-280;285-309;319-337;429-448;478-492 <TK2>
 R/Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
 J. Biol. Chem. 267, 8919-8924, 1992
 A/Title: A calyculin-associated protein is a newly identified member of the Ca(2+)/phosphatase family.
 A/Reference number: A38250; MUID:92250478; PMID:1533622

A/Accession: A38250
 A/Molecule type: Protein
 A/Residues: 104-141;213-223,'X',225-231;254-263;271-280;285-291,'X',293-309
 C/Comment: This protein binds specifically to calyculin in a Ca2+ dependent manner.
 C/Superfamily: annexin VII; annexin repeat homology
 C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phosphatase
 F/201-272/Domain: annexin repeat homology <AX1>
 F/212-228/Region: endonexin fold #status predicted
 F/212-228/Region: endonexin repeat homology <AX2>
 F/273-344/Domain: annexin repeat homology <AX3>
 F/284-300/Region: endonexin fold #status predicted
 F/356-428/Domain: annexin repeat homology <AX3>
 F/368-384/Region: endonexin fold #status predicted
 F/432-503/Domain: annexin repeat homology <AX4>
 F/443-459/Region: endonexin fold #status predicted
 F/58/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.6%; Score 873; DB 1; Length 503;
 Best Local Similarity 54.6%; Pred. No. 5.2e-49;
 Matches 172; Conservative 60; Mismatches 83; Indels 0; Gaps 0;

QY 6 RGVTDPPGFDERADATLRKAMKGLGTDEESILTLTSSNAQOEISAFTLFGRL 65
 DB 189 RGTITDASGFDLRBAEVLKAMKGGTDEQAIIIDCGSRNKORQOILLSPFTAYGKDL 250
 QY 66 LDDKSELGTGFEKLIVALKPSRLYDAVELKALKGAGTNEKVLTEIASSRPEELR 125
 DB 249 IKDLKSELGNFEKTLTALMKTPVLPFAVEIKAIKAGTDEACLEIILASSRNEHIR 310
 QY 126 KOYEEBEGSSLEDVVGTSYQRMVVLQANRDPAGIDEADEVDAQALFOAGEL 185
 DB 309 NRYYKTEFFKLTLEAARSDTSQHPQLLSLQGNBESNTVDMSLVQDVGELVYAG 370
 QY 186 KMGTDDEKFTITGTSVSHLRKVPKMTISGFOIETITDRSGNLQDLAVYKS 245
 DB 369 RLGTDESKFNAVLCSRRALHVAVFNEYQMTGDIKSIKREMSDGLQGLAVVCLK 430
 QY 246 SIPAVLAETLYYAMKAGTDDHTLIRVWSSRSEIDLFNIRKERRKPFATSLYSMIK 305
 DB 429 NTPAFPAERLNKMRGAGTDRTLIRIMVSRSEIDLDIRAERYRLVKGSLYHDITDTS 490

QY 306 GDYKALLLLCGEDD 320
 DB 489 GDYKILLKTCGND 503

RESULT 15
 A53152
 annexin XI - human
 C/Species: Homo sapiens (man)
 C/Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 13-Aug-1995
 R/Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij, W.J.
 J. Biol. Chem. 269, 4240-4246, 1994
 A/Title: The 56K autoantigen is identical to human annexin XI.
 A/Reference number: A53152; MUID:94140847; PMID:7508441
 A/Accession: A53152
 A/Molecule type: preliminary
 A/Status: preliminary
 A/Residues: 1-505 <MS>
 A/Cross-references: GB:L19605; NID:g457128; PIDN:AAA19734.1; PID:g457128
 A/Genetics:
 A/Gene: GDB:ANX11
 A/Cross-references: GDB:113076
 A/Map position: 9q41-q42
 C/Superfamily: annexin VII; annexin repeat homology
 C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein;
 F/203-274/Domain: annexin repeat homology <AX1>
 F/275-346/Domain: annexin repeat homology <AX2>
 F/358-430/Domain: annexin repeat homology <AX3>
 F/434-505/Domain: annexin repeat homology <AX4>

Query Match 54.1%; Score 865; DB 2; Length 505;
 Best Local Similarity 53.7%; Pred. No. 1.7e-48;

Matches 169; Conservative 61; Mismatches 85; Indels 0; Gaps 0;

```

QY 6 RGYTDFPGDEPRDAETLRKAMKGLGTDEESILTLLTSRNSNAOROEISAFKTLFGRDL 65
    |||||
Db 191 RGTITDAGFDPDLDAEVLRRKAMKGFDEQOAIIDCLSRSNKROQLLEFKIAYGKDL 250
QY 66 LDDKSELTKGEKLIYALMKPSRLYDAYELKHALKAGTNEKVTLEIASRTPEELRAI 125
    |||||
Db 251 IKDKSELISGFEKTLTALMTKTPVLPDLYETKEAIKGVGDEACILIELIASRSNEHREL 310
QY 126 KQVVEEYSSSLIEDVVGDTSSGYQRMVLVLQANRPDAGIDEAQVEQDAQALFOAGEL 185
    |||||
Db 311 NRAYKAFPKTLLEAIIASDTSIGHQRLILISQGNRDESTNVDSLAQRDAQELYAAGEN 370
QY 186 KWTDEEKFTITFCTRSVSHLRKVPEDKYMITSQFIETTIDRETSGNLEQLLAVKASIR 245
    |||||
Db 371 RLGTDESKFNVAVLCSRSRAHLVAVFNEYQMTGDIKSLCREMSGLEELMALVAVCLK 430
QY 246 SIPIYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNATSLYSMIKDDTS 305
    |||||
Db 431 NTPAFPFERLNRKMRGAGTDRTLIRIVSRSETDLDIRSEYRMVKGSLVHDSGDS 490
QY 306 GDYKALLLLCGEDD 320
    |||||
Db 491 GDYRKILLKICGAND 505
    |||||

```

RESULT 16

L0H08

annexin VIII - human

N/Alternate names: vascular anticoagulant beta

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999

C/Accession: S06476; A38847

R./Hauptmann, R.; Maurer-Pogoy, I.; Krystek, E.; Bodo, G.; Andree, H.; Reutelingersperger, C.

Eur. J. Biochem. 185, 63-71, 1989

A./Title: Vascular anticoagulant beta: a novel human Ca(2+)/phospholipid binding protein

h VAC-alpha.

A./Reference number: S06476; MUID:90032687; PMID:2530088

A./Accession: S06476

A./Molecule type: mRNA

A./Residues: 1-327 <HAU>

A./Cross-references: EMBL:X16662

A./Note: the sequence from Fig. 3 is inconsistent with that in Fig. 1 in lacking 208-Arg

A./Note: 6-Ala was also found

A./Note: 77-Ala, 80-Ala, 96-Ala, 122-Ala were also found

R./Chang, K.S.; Wang, G.; Freireich, E.J.; Daly, M.; Naylor, S.L.; Trujillo, J.M.; Staas, Blood 79, 1802-1810, 1992

A./Title: Specific expression of the annexin VIII gene in acute promyelocytic leukemia.

A./Reference number: A38847; MUID:92216091; PMID:1313714

A./Accession: A38847

A./Molecule type: mRNA

A./Residues: 1-57, 'T', '59-82, 'U', '84-156, 'S', '158-176, 'G', '178-312, 'RV', '315-327 <CHA>

A./Cross-references: GB:M81844; NID:9178700; PIDN:AA6383.1; PID:9178701

A./Note: the authors translated the codon TTG for residue 83 as Phe, AGT for residue 157

A./Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

dercocoed.

C/Genetics:

A./Gene: GDB:ANX8

A./Cross-references: GDB:128069

A./Map position: 10q11.2-10q11.2

C./Superfamily: annexin I; annexin repeat homology

C./Keywords: calcium binding; duplication; endonexin fold; phospholipid binding

F./2-327/Product: annexin VIII #status predicted <MAT>

F./24-95/Domain: annexin repeat homology <AX1>

F./35-51/Region: endonexin fold #status predicted

F./96-167/Domain: annexin repeat homology <AX2>

F./107-123/Region: endonexin fold #status predicted

F./180-252/Domain: annexin repeat homology <AX3>

F./192-208/Region: endonexin fold #status predicted

F./256-327/Domain: annexin repeat homology <AX4>

F./267-283/Region: endonexin fold #status predicted

Query Match 52.0%; Score 832.5; DB 1; Length 327;
 Best Local Similarity 56.5%; Pred. NO. 1.3e-46;
 Matches 177; Conservative 46; Mismatches 87; Indels 1; Gaps 1;

```

QY 8 TVTDFPGDEPRADAEETLRKAMKGLGTDEESILTLLTSRNSNAOROEISAFKTLFGRLLD 67
    |||||
Db 14 TVSSSHFNPDPAETLYKAMKGLGTNEQAIIVLTSTQROQIAKSTPAQFKDLTE 73
QY 68 DLKSELTKGEKLIYALMKPSRLYDAYELKHALKAGTNEKVTLEIASRTPEELRAIKQ 127
    |||||
Db 74 TLKSELISGFEKRLIYALMPPRYEAKELHDANKGLGTKEGVILEIASRTQRLIMK 133
QY 128 VVEEYSSSLIEDVVGDTSSGYQRMVLVLQANRPD-DAQIDEAQVEQDAQALFOAGELK 186
    |||||
Db 134 AYEDYSSSLIEDVVGDTSSGYQRMVLVLQANRPD-DAQIDEAQVEQDAQALFOAGELK 193
QY 187 KWTDEEKFTITFCTRSVSHLRKVPEDKYMITSQFIETTIDRETSGNLEQLLAVKASIR 246
    |||||
Db 194 RGTDEKFTITLCTRSVSHLRKVPEDKYMITSQFIETTIDRETSGNLEQLLAVKASIR 253
QY 247 IPIYLAETLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNATSLYSMIKDDTS 306
    |||||
Db 254 LHSYFARLYAMKAGTDDHTLIRVWRSSEIDLFNIRKPKNATSLYSMIKDDTS 313
QY 307 DYKALLLLCGEDD 319
    |||||
Db 314 DYKALLSLVGS 326
    |||||

```

RESULT 17

L0H03

annexin III - human

N/Alternate names: 1,2-cyclic-inositol-phosphate phosphodiesterase (EC 3.1.4.36); calcium

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999

C/Accession: A47658; B29250; A41213; B31046; A60707

R./Tait, J.F.; Smith, C.; Xu, L.; Cookson, B.T. Genomics 18, 79-86, 1993

A./Title: Structure and polymorphisms of the human annexin III (ANX3) gene.

A./Reference number: A47658; MUID:94102764; PMID:8276419

A./Accession: A47658

A./Molecule type: DNA

A./Status: translation not shown

A./Residues: 1-323 <RES>

A./Cross-references: GB:L20591; NID:9410200; PIDN:AAA16713.1; PID:9410202

R./Pepinsky, R.B.; Tizard, R.; Matcaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, J. Biol. Chem. 263, 10799-10811, 1988

A./Title: Five distinct calcium and phospholipid binding proteins share homology with 11p

A./Reference number: B29250; MUID:86273202; PMID:2968983

A./Accession: B29250

A./Molecule type: mRNA

A./Residues: 1-323 <PEP>

A./Cross-references: EMBL:M20560; NID:9186367; PIDN:AAA59496.1; PID:9307115; EMBL:J03899

R./Ross, T.S.; Tait, J.F.; Majerus, P.W. Science 248, 605-607, 1990

A./Title: Identity of inositol 1,2-cyclic phosphate 2-phosphohydrolase with 11pocortin II

A./Reference number: A41213; MUID:90239555; PMID:2159184

A./Accession: A41213

A./Molecule type: protein

A./Residues: 41-102; 126-138 <ROS>

R./Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E.; Biochemistry 27, 6268-6276, 1988

A./Title: Placental anticoagulant proteins: isolation and comparative characterization of

A./Reference number: A90344; MUID:89118212; PMID:2975506

A./Accession: B31046

A./Molecule type: protein

A./Residues: 41-79; 85-88; 104-119; 126-128, 'X', '130-145, 'G', '147-153, 'X', '155-157, 'X', '159-160;

J. Clin. Invest. 85, 1065-1071, 1990

A./Title: Purification and characterization of an abundant cytosolic protein from human n

A./Reference number: A60707; MUID:90203211; PMID:2138632

A./Accession: A60707

```

F.194-165/Domain: annexin repeat homology <AX2>
F.105-121/Region: endonexin fold #status predicted
F.177-249/Domain: annexin repeat homology <AX3>
F.188-205/Region: endonexin fold #status predicted
F.189-224/Domain: annexin repeat homology <AX4>
F.253-324/Domain: annexin repeat homology <AX4>
F.264-280/Region: endonexin fold #status predicted
F.202-219/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 49.1%; Score 785; DB 1; Length 324;
Best Local Similarity 48.3%; Pred. No. 1.5e-43;
Matches 152; Conservative 65; Mismatches 98; Indels 0; Gaps

QY 6 RGVTVDFPGFPERDAETLRKRMKGLGTDEESILTLTSRSNAQOEISAFKTLFGKD
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
10 KETINNYGFPNSVDAAEIRAKIGIGDEKTLINILTERSNAQROLIVKQYOEAVEQDA
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 66 LDDLSESLTGKFEKELIVAMKPSRLYDAVELKHALKGKGTNEKVELTILASTPEELRA
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
70 KADIKGLDLSGHEHVMVLTAPAFDGAKKOLKKSRRGKGTEDTLTILTLTTSQOME
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 126 KQVEBERGSSLEDDVVGDTSGYQRMVLVLLQNRDPDAGIDEAQVEEDAAQALFOAG
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 130 SQAYVYAAKKNLRDDISSETSGDFRKALLTLADGGKDESLKYDEHLAKKDAQTLVDAG
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 186 KNGTDEKRTTTRGRSVSHLAKVPDKWTISGFOEETRIDETSGLNEQLLLAAVKS
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 190 KMGTDDEKFTTEILCLNSFPOLKLTPEEYNNISOKDIEDIKGELSHFFEDLLAAVRC
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 246 SIPVLAETLLYAMKAGDGDHLLIKVWVSREIDLFNIRKERKKNFATSLYSMIKGD
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 250 NTPAFPLAGRLHQLKAGTDEFTLRINWRSREIDLLDRREPKKHGCVLSAIGSD
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 306 GDYKALLLLCGEDD 320
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 310 GDYRYVLLKTCGGDD 324
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 19
LNUH07
annexin VII, long form - human
N:Alternate names: syneXin
N:Contains: annexin VII, long form; annexin VII, short form
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence revision 26-Jan-1996 #text_change 22-Jun-1
C:Accession: A54467; A35554; A39513; B39513
R:Shirvan, A.; Srivastava, M.; Wang, M.G.; Cultraro, C.; Magendzo, K.; M
Biochemistry 33, 6888-6901, 1994
A>Title: Divergent structure of the human syneXin (annexin VII) gene and
A:Reference number: A54467; MUID:94264005; PMID:7515686
A:Accession: A54467
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-488 <SH>
A:Burns, A.L.; Magendzo, K.; Shirvan, A.; Srivastava, M.; Rojbas, E.; Ali
Proc. Natl. Acad. Sci. U.S.A. 86, 3798-3802, 1989
A>Title: Calcium channel activity of purified human syneXin and structun
A:Reference number: A32554; MUID:89264510; PMID:2542947
A:Accession: A32554
A:Molecule type: mRNA
A:Residues: 1-145, 168-488 <BUR>
A:Cross-references: EMBL:J04543; NID:G338243; PIDN:AAA3616.1, PID:G338
R:Magendzo, K.; Shirvan, A.; Cultraro, C.; Srivastava, M.; Pollard, H.B
J. Biol. Chem. 266, 3228-3232, 1991
A>Title: Alternative splicing of human syneXin mRNA in brain, cardiac,
A:Accession: A39513; MUID:91131630; PMID:1825209
A:Reference number: A39513
A:Molecule type: mRNA
A:Residues: 137-145, 168-176 <MAG>
A:Cross-references: EMBL:J05732
A:Accession: B39513
A:Molecule type: mRNA
A:Residues: 137-176 <MA2>
C:Comment: Annexin undergo reversible, calcium-dependent binding to me

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deretocod.

C:Comment: The long form of annexin VII is more prevalent in brain, heart, and skeletal

C:Genetics:

A:Gene: GDB:ANX7

A:Cross-references: GDB:369042; OMIM:186360

A:Map position: 10q21.1-10q21.2

A:Introns: 17/3; 87/1; 124/1; 145/3; 167/3; 202/2; 233/3; 271/3; 328/3; 385/3; 411/1; 44

C:Superfamily: annexin VII; annexin repeat homology

C:Keywords: alternative splicing; calcium binding; calcium channel; duplication; endonex

F:1-148/Product: annexin VII, long form #status predicted <MAT>

F:1-145/166-488/Product: annexin VII, short form #status predicted <MA3>

F:188-259/Domain: annexin repeat homology <AX1>

F:199-215/Region: endonexin fold #status predicted

F:260-331/Domain: annexin repeat homology <AX2>

F:271-287/Region: endonexin fold #status predicted

F:343-415/Domain: annexin repeat homology <AX3>

F:355-371/Region: endonexin fold #status predicted

F:419-488/Domain: annexin repeat homology <AX4>

F:430-446/Region: endonexin fold #status predicted

Query Match 48.8%; Score 780; DB 1; Length 488;

Best Local Similarity 48.1%; Pred. No. 5.1e-43;

Matches 153; Conservative 66; Mismatches 99; Indels 0; Gaps 0;

```

QY 1 MAQVLRGTVDTPFGPERADAEITLRKAMKGLGTDESITLTLSRSNAQOEISAAFKTL 60
DB 171 VTQVGTGTRIPANPFAIRPAIRDAELIRKAMGFGTDEQATVAVNRSNDQOKKAFAKTS 230
QY 61 FGRDLDDLKSELGTGFEKLIYALMKPSRLYAYELKHALKGAGTNEKYLTIISRTPE 120
DB 233 YGKDLIKDKLSLGNMELIILALFMPPTYYDMSLRKMGAGTQERVLITLCTRTNQ 290
QY 121 ELRAIKQVVEEYEGSSLEDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVQDAQALF 180
DB 291 ELREIYRCYQSEGRDLEKDIRSDTSGHFERLLVMCGNRRDQSVNMQMAQEAQRIY 350
QY 181 QAGELKMGDEEKEFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQILLAV 240
DB 351 QAGEGLGTDESCFNMILATRSFPOLKATMEAYSRMARDLSSVSRSFGVSGGLKTI 410
QY 241 VKSIRISPAIYLAETIYYAMKAGTDHTLIRVWRSSEIDFNIRKEPKNPAISYMI 300
DB 411 LQCALNRPAPFAERLYAMKAGTDSITLVIRIVTRSSIDLVOIKQMTQVQKTLGIMI 470
QY 301 KGDTSGDYKKAALLLCCGE 318
DB 471 AGDTSGDYRLLLAIVGQ 488

```

RESULT 20

S29170

annexin VII - mouse

N:Alternate names: synexin

C:Species: Mus musculus (house mouse)

C:Date: 25-Feb-1994 #sequence revision 01-Sep-1995 #text_change 13-Aug-1999

C:Accession: S29170; S46209; S51173

R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.

Biochem. J. 289, 735-741, 1993

A:Title: Mouse synexin (annexin VII) polymorphisms and a phylogenetic comparison with ot

A:Reference number: S29170; MUID:93168121; PMID:7916616

A:Accession: S29170

A:Molecule type: mRNA

A:Residues: 1-463 <ZHA>

R:Zhang-Keck, Z.Y.; Srivastava, M.; Kozak, C.A.; Caohuy, H.; Shitvan, A.; Burns, A.L.; F

Biochem. J. 301, 835-845, 1994

A:Title: Genomic organization and chromosomal localization of the mouse synexin gene.

A:Reference number: S46209; MUID:94330961; PMID:8053909

A:Accession: S46209

A:Molecule type: DNA

A:Residues: 1-463 <ZHF>

R:Zhang-Keck, Z.Y.; Burns, A.L.; Pollard, H.B.

submitted to the EMBL Data Library, May 1993

A:Reference number: S51173

A:Accession: S51173

A:Molecule type: mRNA

A:Residues: 1-144, 'S', 146-303, 'A', 305-463 <ZHW>

A:Cross-references: EMBL:L13129; NID:g293293; PIDN:AAA37238.1; PID:g293294

C:Genetics:

A:Gene: MGI:Anx7

A:Cross-references: MGI:88031

A:Map position: 14

A:Introns: 19/3; 87/1; 121/1; 142/3; 177/1; 208/3; 246/3; 303/3; 360/3; 386/1; 423/3

C:Superfamily: annexin VII; annexin repeat homology

C:Keywords: calcium channel; ion channel

F:163-234/Domain: annexin repeat homology <AX1>

F:235-306/Domain: annexin repeat homology <AX2>

F:318-390/Domain: annexin repeat homology <AX3>

F:394-463/Domain: annexin repeat homology <AX4>

Query Match 48.4%; Score 774; DB 2; Length 463;

Best Local Similarity 47.5%; Pred. No. 1.2e-42;

Matches 151; Conservative 68; Mismatches 99; Indels 0; Gaps 0;

```

QY 1 MAQVLRGTVDTPFGPERADAEITLRKAMKGLGTDESITLTLSRSNAQOEISAAFKTL 60
DB 146 MTQGTGTTLPASNFPAMRDAEITLRKAMGFGTDEQATVAVNRSNDQOKKAFAKTM 205
QY 61 FGRDLDDLKSELGTGFEKLIYALMKPSRLYAYELKHALKGAGTNEKYLTIISRTPE 120
DB 206 YGKDLIKDKLSLGNMELIILALFMPPTYYDMSLRKMGAGTQERVLITLCTRTNQ 265
QY 121 ELRAIKQVVEEYEGSSLEDVVGDTSGYYQRMVLVLLQANRPDAGIDEAQVQDAQALF 180
DB 266 ELRIDVRCYQLEFGDRDLEKDIRSDTSGHFERLLVMCGNRRDQSVNMQMAQEAQRIY 325
QY 181 QAGELKMGDEEKEFTITIGTRSVSHLRKVPDKMTISGFOIETTIDRETSNLEQILLAV 240
DB 326 QAGEGLGTDESCFNMILATRSFPOLKATMEAYSRMARDLSSVSRSFGVSGGLKTI 385
QY 241 VKSIRISPAIYLAETIYYAMKAGTDHTLIRVWRSSEIDFNIRKEPKNPAISYMI 300
DB 386 LQCALNRPAPFAERLYAMKAGTDSITLVIRIVTRSSIDLVOIKQMTQVQKTLGIMI 445
QY 301 KGDTSGDYKKAALLLCCGE 318
DB 446 ASDTSGDYRLLLAIVGQ 463

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RESULT 21

L1312

annexin XII - Hydra vulgaris

C:Species: Hydra vulgaris

C:Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 22-Jun-1999

C:Accession: A42660; B42660

R:Schlaepfer, D.D.; Fisher, D.A.; Brandt, M.E.; Bode, H.R.; Jones, J.M.; Haigler, H.T.

J. Biol. Chem. 267, 9529-9539, 1992

A:Title: Identification of a novel annexin in Hydra vulgaris. Characterization, cDNA clo

A:Reference number: A42660; MUID:92250599; PMID:1339458

A:Accession: A42660

A:Molecule type: mRNA

A:Residues: 1-316 <SCH>

A:Cross-references: GB:M83736; NID:g159255; PIDN:AAA29206.1; PID:g159256

A:Accession: B42660

A:Molecule type: protein

A:Residues: 2-9, 'D', 11-30, 246-251, 'E', <SC2>

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

deretocod.

C:Superfamily: annexin I; annexin repeat homology

C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F:2-316/Product: annexin IV #status experimental <MAT>

F:16-87/Domain: annexin repeat homology <AX1>

F:27-43/Region: endonexin fold #status predicted

F:88-159/Domain: annexin repeat homology <AX2>

F:99-115/Region: endonexin fold #status predicted

F:171-243/Domain: annexin repeat homology <AX3>

RESULT 23
 570644
 annexin VII - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Aug-1999
 C/Accession: S70644
 R/Stavitsky, M.; Zhang-Kec, Z. Y.; Caohuy, H.; McPhie, P.; Pollard, H. B.
 Biochem. J. 316, 729-735, 1996
 A/Title: Novel isoforms of synexin in Xenopus laevis: multiple tandem PEGM repeats dist
 A/Reference number: S70644; MUID:96265035; PMID:8670145
 A/Accession: S70644
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-512 <SR>
 A/Cross-references: EMBL:U16365; NID:G790543; PIDN:AA18145.1; PID:G790544
 C/Superfamily: annexin VII; annexin repeat homology
 F/212-282/Domain: annexin repeat homology <AX1>
 F/283-355/Domain: annexin repeat homology <AX2>
 F/367-439/Domain: annexin repeat homology <AX3>
 F/443-512/Domain: annexin repeat homology <AX4>

Query Match 44.1%; Score 706; DB 2; Length 512;
 Best Local Similarity 47.3%; Pred. No. 3.2e-38;
 Matches 146; Conservative 60; Mismatches 103; Indels 2; Gaps 2;

QY 6 RGIVTDFPGDERADAEITRKAMKGLTDEESITLTLSRSNAQOEISAFAFKTLFPRDL 65
 Db 200 QGITKAPNFDALSDAEKTRKAMKGFIDEKPI-DVYANSNDROKIOAFAFKAYAKDL 258
 QY 66 LDDLSKSLTGKFEKLIYALMKPSRLYDAVELKHALKAGATNEKYLTEIIASFTPEELRAI 125
 Db 259 IKDLKSLSGNVEELITLALFMPSTYYDAMSLYNNMKAGQGERVLIILCTFNTSELRNI 318
 QY 126 KQYEEYEGSSLEDVDVGTSGYQRMV-VLQANDPDAGIDEAIVEDPAQALPAGE 184
 Db 319 VACTKQFGEIEKIDRSDTSGHERLLISIMAGIYDESQNVMOQAEODAPRLYQAGE 378
 QY 185 LKMGTEDEKFTITFGTSVSHLRKVPDKWMTISGFOIEETIDETSQNLLEQLLAVKSI 244
 Db 379 GKIGTBESSNVLASISFQOLKAVAEARISIRDLISVIGREFSGYEDGKAVLQCA 438
 QY 245 RSIIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKAFATSLVMTKGDPT 304
 Db 439 INNPFLFRDLCSMGKAGDDBTLIRITVTRSEIDLVOIKAYVQYQKSLSAALISDT 498
 QY 305 SGDYKXKALLILLC 317
 Db 499 SGAYKRMLLAISG 511

RESULT 24
 S41022
 hypothetical protein T07C4.9 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C/Accession: S41022
 R/Berks, M.
 submitted to the EMBL Data Library, January 1994
 A/Reference number: S41014
 A/Accession: S41022
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-676 <BER>
 A/Cross-references: EMBL:Z29443; NID:g1067051; PID:g443836
 C/Genetics:
 A/Introns: 69/3; 161/1; 208/3; 227/1; 357/1; 505/3
 C/Superfamily: annexin repeat homology
 F/373-444/Domain: annexin repeat homology <AX1>
 F/445-516/Domain: annexin repeat homology <AX2>
 F/528-600/Domain: annexin repeat homology <AX3>
 F/604-675/Domain: annexin repeat homology <AX4>

Query Match 44.1%; Score 706; DB 2; Length 676;
 Best Local Similarity 46.5%; Pred. No. 4.5e-38;
 Matches 146; Conservative 63; Mismatches 103; Indels 2; Gaps 1;

QY 4 VLRGTVDFF-GPERADAEITRKAMKGLTDEESITLTLSRSNAQOEISAFAFKTLF 61
 Db 357 VMICTPSVFPGVQNSNADAEVLKAMKGLGNNKSYISILCORTNOROEISAFAFKMY 416
 QY 62 GRDILDDKSELTKGFEKLIYALMKPSRLYDAVELKHALKAGATNEKYLTEIIASFTPEE 121
 Db 417 GKDLIKELKGLHGDFFDILLALMDAPAIADAKQHLHMGSLGKESVLEIMTSKRNQ 476
 QY 122 LRAIKQYEEYEGSSLEDVDVGTSGYQRMVLLQANDPDAGIDEAIVEDPAQALFQ 181
 Db 477 IQQVRDAYKMLFKXDLERDLIGETSGHFKRLVSLCAGRDESSQDTGLANDARLLQ 536
 QY 182 AGEKMTDEKFTITGTSVSHLRKVPDKWMTISGFOIEETIDETSQNLLEQLLAVV 241
 Db 537 AGEKRLDTESTNAIILASQNFQSLRVFEYQKASNHSIEKALIEFPGSDIRIGLLAVI 596
 QY 242 KSIPIPAYLAETLYYAMKAGTDDHTLIRVMVSRSEIDLFNIRKFRKAFATSLVSMIK 301
 Db 597 AVIRNRPAYFAKLLHDSMKGLGTRDNDLRLCVTRAEDMGDIRMFQSLYRTSLNEMIK 656
 QY 302 GDTSGDYKXKALLIL 315
 Db 657 GDSCGAYKEGLIAL 670

RESULT 25
 LUBO36
 annexin II - bovine
 N/Alternate names: 36k protein; calcium-dependent phospholipid-actin-binding protein; ca
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 04-Dec-1986 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
 R/Kristensen, T.; Saris, C. J. M.; Hunter, T.; Hicks, L. J.; Noonan, D. J.; Glenney Jr., J. R.
 Biochemistry 25, 4497-4503, 1986
 A/Title: Primary structure of bovine calpactin I heavy chain (p36), a major cellular sub
 A/Reference number: A03081; MUID:87026517; PMID:2945590
 A/Accession: A03081
 A/Molecule type: protein
 A/Residues: 1-339 <KRI>
 A/Cross-references: GB:M14056; NID:G162778; PIDN:AAA0421.1; PID:G162779
 A/Experimental source: Madin-Darby kidney cell line MDCK
 R/Martin, F.; Derancourt, J.; Capony, J. P.; Watrin, A.; Cavadore, J. C.
 Biochem. J. 251, 777-785, 1988
 A/Title: A 36 kDa monomeric protein and its complex with a 10 kDa protein both isolated
 n-severing properties.
 A/Reference number: S02477; MUID:88326216; PMID:2970844
 A/Accession: S02477
 A/Molecule type: protein
 A/Residues: 27-61 <MAR>
 A/Experimental source: aorta
 A/Note: 44-Lys was also found
 R/Glenney Jr., J. R.; Boudreau, M.; Galyean, R.; Hunter, T.; Tack, B.
 J. Biol. Chem. 261, 10485-10488, 1986
 A/Title: Association of the S-100-related calpactin I light chain with the NH2-terminal
 A/Reference number: A3844; MUID:86278112; PMID:2942542
 A/Contents: annotation; amino-terminal acetylation
 C/Comment: Annexin undergo reversible, calcium-dependent binding to membrane phospholip
 derstood.
 C/Comment: Calpactin I, a tetramer of two heavy chains and two light chains, is found in
 skeleton and be involved with exocytosis.
 n I binds two moles of calcium ion per mole of annexin II. These ligands make annexin II
 C/Comment: Annexin II may act as a regulator of intracellular phospholipase activity.
 C/Superfamily: annexin I; annexin repeat homology
 C/Keywords: acetylated amino end; actin binding; calcium binding; duplication; endonexin
 F/2-339/Product: annexin II #status experimental <MKT>
 F/2-12/Region: calpactin I light chain binding #status predicted
 F/36-107/Domain: annexin repeat homology <AX1>

F;47-63/Region: endonexin fold #status predicted
F;108-179/Domain: annexin repeat homology <AX2>
F;119-135/Region: endonexin fold #status predicted
F;192-264/Domain: annexin repeat homology <AX3>
F;204-320/Region: endonexin fold #status predicted
F;268-339/Domain: annexin repeat homology <AX4>
F;279-295/Region: endonexin fold #status predicted
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F;24/Binding site: phosphate (Tyr) (covalent) #status predicted
F;26/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 44.0%; Score 704.5; DB 1; Length 339;
Best Local Similarity 46.3%; Pred. No. 2,4e-38;
Matches 146; Conservative 62; Mismatches 106; Indels 1; Gaps 1;

QY 7 GTVDFPQGFDERADAEITLRKAMKGLGTDEESITLTLTSRSNAQOEISAFFETLFGRDLL 66
Db 25 GSVKAYTNFDEARDLNIETAIKTGVDEVTIVNLTNRSNQRODIAFAVQRTKEIA 84
QY 67 DDLKSELTKGFEKLIIVALKMPSRLYDAVELKHALKAGTNEKVLTEIIASRTPEELRAIK 126
Db 85 SALKSALSGHLETVILGLKTPAQYDASELKASKMKGAGTDEDSLIEIICSRTNOELQELIN 144
QY 127 QYEEYEGSSLEDVVGDTSGYYQRMVLVLLQANDPDAG-IDEAQVEDQAQLFOAGEL 185
Db 145 RYKEMTKTDLEKDIVSDTSGDPRKLMVALAKGRAEDGSVIDYELIDQDARDLYDAGVK 204
QY 186 KMGTEBEKFTITFGTNSVSHLRKVPDKMTISGFOIEETIDRETSNLEQLLAVVKSIR 245
Db 205 RKGTDPKMWISINTERSVCHLQKQFERKYSYSPYDMLSEIKKEVGDLLENAPINLVQCIQ 264
QY 246 SIPATLAETLYAMKAGCDHDLIIVMSRSEIDLFINIKERKNPATSLYSMIKGDT 305
Db 265 NKPLYPADRLYDMKGGTQKVLIRIMWSRSEVDMKLTSEFKKYGKSLYYIIGQDTK 324
QY 306 GDYKALLLLCGEED 320
Db 325 GDYQKALLLYCGGDD 339

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Job time : 22 secs

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